

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2006, 13:50:01 ; Search time 218.657 Seconds
(without alignments)
753.540 Million cell updates/sec

Title: US-10-799-943-2
Perfect score: 2009
Sequence: 1 MSHKGSVVAQNGAPASNR.....SNLQFRYCLEGGCTDITLL 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2009	100.0	375	4	AAB74699
2	2009	100.0	375	4	AAM78650 Human mem
3	2009	100.0	375	5	ABB89913 Human pol
4	2009	100.0	375	8	ADQ37764 Human adi
5	2009	100.0	375	9	ADW24159 Human adi
6	2009	100.0	375	9	ADZ00539 Human adi
7	2005	99.8	379	4	AAM79634 Human pro
8	1998	99.5	375	4	AAB93005 Human pro
9	1970	98.1	370	6	ABB99648 Amino aci
10	1967	97.9	375	9	ADW24313 Rat Adipo
11	1954	97.3	375	8	ADQ37768 Mouse adi
12	1954	97.3	375	9	ADW24160 Murine Ad
13	1696	84.4	387	4	AAU30936 Novel hum
14	1529	76.1	381	9	ADW24251 Human adi
15	1403.5	69.9	386	8	ADR09023 Human pro
16	1403.5	69.9	386	8	ADR10196 Human pro
17	1403.5	69.9	386	8	ADS98076 Protein f
18	1403.5	69.9	386	8	ADU76417 Progesterin
19	1391.5	69.3	386	9	ADW24156 Murine Ad
20	1378.5	68.6	386	9	ADW24315 Rat Adipo
21	1378	68.6	311	8	ADQ37770 Mouse adi
22	1378	68.6	311	9	ADW24162 Murine Ad
23	1378	68.6	311	9	ADW24397 Murine Ad
24	1376	68.5	421	9	ADW24253 Human Adi

25	1359	67.6	386	9	ADW24154	Adw24154 Human Adi
26	1347	67.0	299	8	ADQ37766	Adq37766 Human adi
27	1345	66.9	299	8	ADW24161	Adw24161 Human Adi
28	1344	66.9	299	6	ABO01308	AbO01308 Human pro
29	1291	64.3	299	8	ADN95988	Adn95988 Human NOV
30	1121	55.8	258	6	ABB99647	Abb99647 Amino aci
31	1121	55.8	258	8	ADU06670	Adu06670 Novel bro
32	1121	55.8	258	9	ADZ09443	Adz09443 Human Adi
33	1117	55.6	258	4	AAM79290	Aam79290 Human pro
34	1075	53.5	201	6	ADA57272	Ada57272 Human sec
35	1075	53.5	201	6	ADA41153	Ada41153 Human sec
36	1075	53.5	201	7	ADC74358	Adc74358 Human sec
37	1075	53.5	201	7	ADD37995	Adel1759 Human sec
38	1075	53.5	201	7	ADZ09443	Adz09443 Human Adi
39	1075	53.5	201	3	ADZ09443	Adz09443 Human Adi
40	1052.5	52.4	288	6	ABB99649	Abb99649 Amino aci
41	1052.5	52.4	288	9	ADW24158	Adw24158 Human Adi
42	1016.5	50.6	444	4	ABB61417	Abb61417 Drosophil
43	1001.5	49.9	322	4	ABB66248	Abb66248 Drosophil
44	328	46.2	218	4	AAM80274	Aam80274 Human pro
45	928	46.2	218	8	ADS98656	Ads98656 Protein f

ALIGNMENTS

RESULT 1
AAB74699
ID AAB74699 standard; protein; 375 AA.
XX
AC AAB74699;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-5.
XX
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US022315.
XX
PR 17-AUG-1999; 99US-0149641P.
PR 09-NOV-1999; 99US-0164203P.
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX
PF 2001-168860/17.
XX
DR N-PSDB; AAF81745.
XX
PT Isolated polypeptide with a human membrane associated protein sequence is
PT useful for the diagnosis, prevention and treatment of cell proliferative,
PT autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX
PS Claim 1; Page 118; 173pp; English.
XX
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition

CC associated with decreased expression of functional MEMAP and antagonists
 CC of MEMAP are used to treat a disease or condition associated with
 CC overexpression of functional MEMAP. These disorders include cell
 CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
 CC disorders. The MEMAP polynucleotides and proteins are also used for the
 CC diagnosis of these disorders. Specific examples of these disorders
 CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
 CC MEMAP proteins can be used to screen for compounds which specifically
 CC bind MEMAP including antibodies, oligonucleotides, proteins and small
 CC molecules. MEMAP polynucleotides can be used to prepare transgenic
 CC animals which can be studied to provide information concerning human
 CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
 CC detection of MEMAP protein and can be used as antagonists to treat or
 CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
 CC can be delivered to target cells with genetic abnormalities with respect
 CC to the expression of MEMAP to treat or prevent a disorder associated with
 CC MEMAP
 CC
 XX
 SQ Sequence 375 AA;

Query Match 100.0%; Score 2009; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-214;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQBE 60
 DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQBE 60

QY 61 EEEVRVLTLPQAHAMKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120
 DB 61 EEEVRVLTLPQAHAMKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120

QY 121 FRACFKSIFRIHTETGNITWLLGFLVFLPLGLTLMRPNNYFMAPLQKVVFGMFFLGA 180
 DB 121 FRACFKSIFRIHTETGNITWLLGFLVFLPLGLTLMRPNNYFMAPLQKVVFGMFFLGA 180

QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYYSFCSPQRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYYSFCSPQRLIYLS 240

QY 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGOM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGOM 300

QY 301 GWFFLMVMYITGAGLYAARIPEPFPGKFDIMFQSHQIFHVLVVAFAFVHFYGVSNLQE 360
 DB 301 GWFFLMVMYITGAGLYAARIPEPFPGKFDIMFQSHQIFHVLVVAFAFVHFYGVSNLQE 360

QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDTL 375

RESULT 2
 AAM78650
 ID AAM78650 standard; protein; 375 AA.
 XX
 AC AAM78650;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1312.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 OS
 XX Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 XX 09-AUG-2001.
 PD

XX 05-FEB-2001; 2001WO-US004098.
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 19-JUL-2000; 2000US-00598075.
 PR 01-SEP-2000; 2000US-00620325.
 PR 15-SEP-2000; 2000US-00654936.
 PR 20-OCT-2000; 2000US-00663561.
 PR 30-NOV-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren P, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK51783.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 3561-3562; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 375 AA;

Query Match 100.0%; Score 2009; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-214;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQBE 60
 DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRVIANPPKABEEQTCVPQBE 60

QY 61 EEEVRVLTLPQAHAMKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120
 DB 61 EEEVRVLTLPQAHAMKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPS 120

QY 121 FRACFKSIFRIHTETGNITWLLGFLVFLPLGLTLMRPNNYFMAPLQKVVFGMFFLGA 180
 DB 121 FRACFKSIFRIHTETGNITWLLGFLVFLPLGLTLMRPNNYFMAPLQKVVFGMFFLGA 180

QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYYSFCSPQRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYYSFCSPQRLIYLS 240

QY 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGOM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGOM 300

QY 301 GWFFLMVMYITGAGLYAARIPEPFPGKFDIMFQSHQIFHVLVVAFAFVHFYGVSNLQE 360
 DB 301 GWFFLMVMYITGAGLYAARIPEPFPGKFDIMFQSHQIFHVLVVAFAFVHFYGVSNLQE 360

QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDTL 375

RESULT 3
 ID ABB89913 standard; protein; 375 AA.
 XX ABB89913;
 AC ABB89913;
 DT 24-MAY-2002 (first entry)
 XX Human polypeptide SEQ ID NO 2289.
 DE
 DE
 DE
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200190304-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 19-MAY-2001; 2001WO-US016450.
 XX
 PR 19-MAY-2000; 2000US-0205515P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Birse CE, Rosen CA;
 XX
 XX WPI; 2002-122018/16.
 DR N-PSDB; ABL90322.
 DR
 DR
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 XX Claim 11; SEQ ID NO 2289; 2081pp + Sequence Listing; English.
 PS
 XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 375 AA;
 Query Match 100.0%; Score 2009; DB 5; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-214;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVQAQNGAPASREADTVLAEGLPGLLEEKGRKRVIANPPKAESEQCPVPQEE 60
 DB 1 MSHKGSVQAQNGAPASREADTVLAEGLPGLLEEKGRKRVIANPPKAESEQCPVPQEE 60
 QY 61 EEEVRVLTPLQAHAMKEEFYKVGGRWRVVPYDVLFDMLKONDYLLHGRPPMPS 120
 DB 61 EEEVRVLTPLQAHAMKEEFYKVGGRWRVVPYDVLFDMLKONDYLLHGRPPMPS 120

QY 121 PRACEKSIPIRIHTETGNIWTHLLGFVLFLFLGILTMLRPNNYFMAPLOEKVVFGMFFLGA 180
 DB 121 PRACEKSIPIRIHTETGNIWTHLLGFVLFLFLGILTMLRPNNYFMAPLOEKVVFGMFFLGA 180
 QY 181 VLCLSFSLFWLFTVYCHSEKSVRTFSKLDYSGLIALLMGSFVFWLWYYSFYCSPQRLIYLS 240
 DB 181 VLCLSFSLFWLFTVYCHSEKSVRTFSKLDYSGLIALLMGSFVFWLWYYSFYCSPQRLIYLS 240
 QY 241 IVCVLGISAIIVQWDRFATPKHROTTRAGVFLGLGLSGVVPVTHFTIABGFVKATTVGOM 300
 DB 241 IVCVLGISAIIVQWDRFATPKHROTTRAGVFLGLGLSGVVPVTHFTIABGFVKATTVGOM 300
 QY 301 GHFFLMAVMIYTGAGLYAARIPEPFGKFDIWFQSHQIFHVLVVAAPVHFVGVSNLOE 360
 DB 301 GHFFLMAVMIYTGAGLYAARIPEPFGKFDIWFQSHQIFHVLVVAAPVHFVGVSNLOE 360
 QY 361 FRYGLEGGCTDDTLL 375
 DB 361 FRYGLEGGCTDDTLL 375
 RESULT 4
 ADQ37764
 ID ADQ37764 standard; protein; 375 AA.
 XX ADQ37764;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human adiponectin receptor AdipoR1 protein SEQ ID NO:2.
 XX
 KW adiponectin receptor; adiponectin binding; human; AdipoR1.
 XX
 OS Homo sapiens.
 XX
 PN WO2004061108-A1.
 XX
 PD 22-JUL-2004.
 XX
 PF 12-JUN-2003; 2003WO-JP007515.
 XX
 PR 29-DEC-2002; 2002JP-00383738.
 XX
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX (NISC) NISSAN CHEM IND LTD.
 XX
 PI Kadowaki T, Yamauchi T, Nagai R, Kamon J;
 XX WPI; 2004-543879/52.
 DR N-PSDB; ADQ37763.
 XX
 PT New protein having adiponectin binding capacity, useful for screening
 PT ligand, agonist or antagonist with respect to adiponectin receptor.
 XX
 PS Claim 1; SEQ ID NO 2; 122pp; Japanese.
 XX
 XX The present invention describes an adiponectin receptor protein (I)
 CC having adiponectin binding capacity, and having a sequence of 375, 299,
 CC 375, or 311 amino acids (S1, see SEQ ID NO:2, 4, 6 and 8 (ADQ37764,
 CC ADQ37766, ADQ37768 and ADQ37770)), or a protein which has one or more
 CC amino acid deletion, substitution or addition in (S1). Also described:
 CC (1) a gene (II) encoding (I); (2) a recombinant vector (III) containing
 CC (II); (3) a transformed host (IV) containing (III); (4) an antibody which
 CC reacts with (I) or its fragment; and (5) a kit for screening a ligand, an
 CC agonist or an antagonist with respect to adiponectin receptor, comprising
 CC any one of (I)-(IV). (I) is useful for screening a ligand, an agonist or
 CC an antagonist of adiponectin receptor, which involves contacting the test
 CC substance with (I). The present sequence represents the human adiponectin
 CC receptor AdipoR1, which is used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 375 AA;

Query Match	100.0%;	Score 2009;	DB 8;	Length 375;	
Best Local Similarity	100.0%;	Pred. No. 2.4e-214;			
Matches 375;	Conservative	0;	Mismatches	0;	Indels
QY	1	MSSHKGSVVQAQNGAPASNRADTVLAEGLPDLLEKGRVIANPPKABEEQTCVPQEE	60		
DB	1	MSSHKGSVVQAQNGAPASNRADTVLAEGLPDLLEKGRVIANPPKABEEQTCVPQEE	60		
QY	61	EEVRVLTLPLOAHAMEKEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGRPPMPS	120		
DB	61	EEVRVLTLPLOAHAMEKEEFVYKWEGRWVPIYDVLDPWLKNDYLLHGRPPMPS	120		
QY	121	FRACFKSIFRIHTETGNIWTHLLGFVFLFLGILTLMLRNPMYFMAPLQKVFVGFGLGA	180		
DB	121	FRACFKSIFRIHTETGNIWTHLLGFVFLFLGILTLMLRNPMYFMAPLQKVFVGFGLGA	180		
QY	181	VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYFVCSQPRLIYLS	240		
DB	181	VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYFVCSQPRLIYLS	240		
QY	241	IVCVLGISAIIVAOQWDRFATPKHROTFRAGVFLGLSLGVVPTMHTIAEGFVKATTVGOM	300		
DB	241	IVCVLGISAIIVAOQWDRFATPKHROTFRAGVFLGLSLGVVPTMHTIAEGFVKATTVGOM	300		
QY	301	GWFFLMVMYITGAGLYAARIPIERFPCKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE	360		
DB	301	GWFFLMVMYITGAGLYAARIPIERFPCKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE	360		
QY	361	FRYGLEGGCTDDTL 375			
DB	361	FRYGLEGGCTDDTL 375			
RESULT 5					
ADW24159					
ID	ADW24159	standard; protein; 375 AA.			
XX	AC	ADW24159;			
XX	DT	24-MAR-2005 (first entry)			
XX	DE	Human AdipoR1 (adiponectin receptor 1) protein.			
XX	KW	antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen-;			
XX	KW	cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;			
XX	KW	cytostatic; virucide; antithyroid; metabolic; anabolic;			
XX	KW	eating-disorders-gen.; metabolic disorder; inflammation;			
XX	KW	cardiovascular disease; nutritional disorder; obesity;			
XX	KW	insulin dependent diabetes; non-insulin dependent diabetes;			
XX	KW	insulin resistance; myocardial infarction; cardiac failure;			
XX	KW	atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;			
XX	KW	hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;			
XX	KW	viral infection; AdipoR1; adiponectin receptor 1.			
XX	OS	Homo sapiens.			
XX	PN	WO2005001061-A2.			
XX	XX	06-JAN-2005.			
XX	XX	24-JUN-2004; 2004WO-US020399.			
XX	PF	25-JUN-2003; 2003US-0482324P.			
XX	PR	10-JUL-2003; 2003US-0486036P.			
XX	PR	04-AUG-2003; 2003US-0492470P.			
XX	PR	02-OCT-2003; 2003US-0508225P.			
XX	PR	11-MAR-2004; 2004US-0552084P.			
XX	XX	(BRIM) BRISTOL-MYERS SQUIBB CO.			
XX	PA	Chen J, Wu S, Lee N;			
XX	PI				
XX	XX				

RESULT 6

ADZ00539
 ID ADZ00539 standard; protein; 375 AA.
 XX
 AC ADZ00539;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE Human AdipoR1.
 XX
 KW Cardiant; Dermatological; Gastrointestinal; Hemostatic; Respiratory-Gen;
 KW Nootropic; Neuroprotective; Uropathic; Cytostatic; Antiinflammatory;
 KW AdipoR1-inhibitor; AdipoR1-activator; G protein coupled receptor;
 KW AdipoR1; receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2005031346-A2.
 XX
 PD 07-APR-2005.
 XX
 PF 16-SEP-2004; 2004WO-EP010384.
 XX
 PR 27-SEP-2003; 2003EP-00021897.
 XX
 PA (FARB) BAYER HEALTHCARE AG.
 XX
 PI Golz S, Brueggemeier U, Geerts A;
 XX
 DR WPI; 2005-254243/26.
 DR N-PSDB; ADZ00538.
 XX
 PT Screening for therapeutic agents useful for treating cardiovascular,
 PT dermatological, respiratory or neurological diseases, cancer or
 PT inflammation in a mammal comprises contacting a test compound with a
 PT AdipoR1 polypeptide.
 XX
 PS Disclosure; SEQ ID NO 2; 135pp; English.
 XX
 CC This sequence represents the G protein coupled receptor, AdipoR1. The
 CC method of the invention for screening for therapeutic agents useful for
 CC treating cardiovascular, dermatological, gastroenterological,
 CC hematological, respiratory, neurological or urological diseases, cancer
 CC or inflammation in a mammal comprises contacting a test compound with an
 CC AdipoR1 polypeptide and detecting binding of the test compound to the
 CC AdipoR1 polypeptide. A further method is included for diagnosing any of
 CC the diseases cited above in a mammal comprising determining the amount of
 CC an AdipoR1 polynucleotide in a sample taken from the mammal and
 CC determining the amount of AdipoR1 polynucleotide in healthy and/or
 CC diseased mammals. Regulators of AdipoR1 activity are useful for
 CC regulating AdipoR1 activity in a mammal having such diseases.
 XX
 SQ Sequence 375 AA;

Query Match 100.0%; Score 2009; DB 9; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-214;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVAQNGAPASNREADTVLAEGLPLEEKGRVIANPPKAESEQCPVPQEE 60
 DB 1 MSHKGSVAQNGAPASNREADTVLAEGLPLEEKGRVIANPPKAESEQCPVPQEE 60
 QY 61 EEEVRVLTFLQAHAMKEEFYKVGWRVVPYDVLPDWLKONDYLLHGRPMPS 120
 DB 61 EEEVRVLTFLQAHAMKEEFYKVGWRVVPYDVLPDWLKONDYLLHGRPMPS 120
 QY 121 FRACFKSIFRIHTETGNITWHLGFLVFLFLGILTMLRPNMYFAPLQEKVFGMFLGA 180
 DB 121 FRACFKSIFRIHTETGNITWHLGFLVFLFLGILTMLRPNMYFAPLQEKVFGMFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVFCSPQRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVFCSPQRLIYLS 240

DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLWYVFCSPQRLIYLS 240
 QY 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGLGLSGVVPFMHFTIABGFVKATVGM 300
 DB 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGLGLSGVVPFMHFTIABGFVKATVGM 300
 QY 301 GWFFLMAVMIITGAGLYAARIPEPFPGKFDIFQSHQIFHVLVVAARFVHFVGSNLOE 360
 DB 301 GWFFLMAVMIITGAGLYAARIPEPFPGKFDIFQSHQIFHVLVVAARFVHFVGSNLOE 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDTL 375
 RESULT 7
 AAM79634
 ID AAM79634 standard; protein; 379 AA.
 XX
 AC AAM79634;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3280.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR N-PSDB; AAK52767.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 300; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and/or
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the

CC sequence listing were missing at the time of publication

XX SQ Sequence 379 AA;

Query Match 99.8%; Score 2005; DB 4; Length 379;

Best Local Similarity 99.7%; Pred. No. 6.7e-214;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILKEKGRVIANPPKAEETCTCPVPOEE 60

DB 5 MSSHKGSVVAQNGAPASNRADTVLAEGLPILKEKGRVIANPPKAEETCTCPVPOEE 64

QY 61 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGRPPMPES 120

DB 65 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGRPPMPES 124

QY 121 FRACPKSIFRIHTETGNIWTHLGLFVLFLGLILTMLRPNNYFMAPLQEKVFGMFFLGA 180

DB 125 FRACPKSIFRIHTETGNIWTHLGLFVLFLGLILTMLRPNNYFMAPLQEKVFGMFFLGA 184

QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240

DB 185 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 244

QY 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 300

DB 245 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 304

QY 301 GWFFLMVMYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360

DB 305 GWFFLMVMYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 364

QY 361 FRYGLEGGCTDDTLL 375

DB 365 FRYGLEGGCTDDTLL 379

RESULT 8

AAB93005

ID AAB93005 standard; protein; 375 AA.

XX AC

XX AAB93005;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:11749.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isozaki T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Iehii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-

XX length cDNAs defined in the specification, and for the detection and/or

XX diagnosis of the abnormality of the proteins encoded by the full-length

PT CDNAs.

XX Claim 8; SEQ ID NO 11749; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialized methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX SQ Sequence 375 AA;

Query Match 99.5%; Score 1998; DB 4; Length 375;

Best Local Similarity 99.7%; Pred. No. 4e-213;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILKEKGRVIANPPKAEETCTCPVPOEE 60

DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILKEKGRVIANPPKAEETCTCPVPOEE 60

QY 61 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGRPPMPES 120

DB 61 EEEVRVLTLPLOAHAMEKEEFYKVGGRWRVPIYDVLPOWLKNDYLLHGRPPMPES 120

QY 121 FRACPKSIFRIHTETGNIWTHLGLFVLFLGLILTMLRPNNYFMAPLQEKVFGMFFLGA 180

DB 121 FRACPKSIFRIHTETGNIWTHLGLFVLFLGLILTMLRPNNYFMAPLQEKVFGMFFLGA 180

QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240

DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240

QY 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 300

DB 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGGFVKATTVGQM 300

QY 301 GWFFLMVMYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360

DB 301 GWFFLMVMYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQOE 360

QY 361 FRYGLEGGCTDDTLL 375

DB 361 FRYGLEGGCTDDTLL 375

RESULT 9

AAB99648

ID AAB99648 standard; protein; 370 AA.

XX AC

XX AAB99648;

XX 28-MAR-2003 (first entry)

XX Amino acid sequence GI7705761 related to FLJ nucleic acids.

XX FLJ; p53 pathway; cancer; G113375715.

XX

XX OS Homo sapiens.

XX FH Key

XX Domain Location/Qualifiers

FT 119..356 /note= "UPF0073 domain"

FT 135..157 /note= "transmembrane domain"

FT 172..194 /note= "transmembrane domain"

FT 207..226 /note= "transmembrane domain"

FT 236..255 /note= "transmembrane domain"

FT 268..287 /note= "transmembrane domain"

FT 297..319 /note= "transmembrane domain"

FT 339..356 /note= "transmembrane domain"

XX WO200298898-A2.

PN 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US017459.

XX 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

PI WPI; 2003-129570/12.

XX Identifying FLJ-specific modulating agents useful for diagnosing or

PT treating disorders associated with defective p53 function, e.g. cancer,

PT comprises comparing a test agent-biased activity and a reference activity

PT in an assay.

XX Example; Page 52-53; 54pp; English.

XX The present sequence represents a polypeptide sequence which is related

XX to FLJ nucleic acids. Genes that modify the p53 pathway in Drosophila are

XX referred to as FLJ. The specification describes a method for identifying

XX candidate p53 pathway modulating agents. The method comprises providing

XX assay system with purified FLJ polypeptide/nucleic acid or their active

XX fragment/derivative; contacting the system with test agent where, in the

XX presence of the agent, the system provides a reference activity; and

XX detecting test agent-biased activity, where differences between test

XX agent-biased activity and reference activity identifies a candidate. The

XX method is useful in identifying a candidate p53 pathway modulating agent,

XX such as a human FLJ gene, that acts as therapeutic or diagnostic targets

XX for disorders associated with defective p53 function, such as cancer

XX Sequence 370 AA;

Query Match 98.1%; Score 1970; DB 6; Length 370;

Best Local Similarity 100.0%; Pred. No. 5.2e-210;

Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSHKGSVVAQGNAPASNREADTVLAEILGPLEEKGVIANPPKAESEQTCVPQEE 60

Db 1 MSHKGSVVAQGNAPASNREADTVLAEILGPLEEKGVIANPPKAESEQTCVPQEE 60

Qy 61 EEEVRVLTLPLOAHAMKKEEFYKVGWGRWRVPIPDVLPDMLKONDYLLHGRPPMPS 120

Db 61 EEEVRVLTLPLOAHAMKKEEFYKVGWGRWRVPIPDVLPDMLKONDYLLHGRPPMPS 120

Qy 121 FRACFKSIFRIHTETGNIWTHLLGFVLFILGILTMLRPNNYFMFAPLQEKVFGVGMFFLGA 180

Db 121 FRACFKSIFRIHTETGNIWTHLLGFVLFILGILTMLRPNNYFMFAPLQEKVFGVGMFFLGA 180

Qy 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALIMGSEFVPLWLYSFYCSQPRLIYLS 240

Db 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALIMGSEFVPLWLYSFYCSQPRLIYLS 240

Qy 241 IVCVLGISALIIVAQWDRFATPKHRTAGVFLGLSGVVPVTHFTIAGGFVKATTVGOM 300

Db 241 IVCVLGISALIIVAQWDRFATPKHRTAGVFLGLSGVVPVTHFTIAGGFVKATTVGOM 300

Qy 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE 360

Db 301 GWFFLMAVMYITGAGLYAARIPEPFPGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE 360

Qy 361 FRYGLEGG 368

Db 361 FRYGLEGG 368

RESULT 10

ADW24313

ID ADW24313 standard; protein; 375 AA.

XX AC ADW24313;

XX DT 24-MAR-2005 (first entry)

XX Rat AdipoR1 (adiponectin receptor 1) protein.

XX antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen.;

XX cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;

XX cytostatic; virucide; antithyroid; metabolic; anabolic;

XX eating-disorders-gen.; metabolic disorder; inflammation;

XX cardiovascular disease; nutritional disorder; obesity;

XX insulin dependent diabetes; non-insulin dependent diabetes;

XX insulin resistance; myocardial infarction; cardiac failure;

XX atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;

XX hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;

XX viral infection; AdipoR1; adiponectin receptor 1.

XX Rattus sp.

XX WO2005001061-A2.

XX 06-JAN-2005.

XX 24-JUN-2004; 2004WO-US020399.

XX 25-JUN-2003; 2003US-0482324P.

PR 10-JUL-2003; 2003US-0486036P.

PR 04-AUG-2003; 2003US-0492470P.

PR 02-OCT-2003; 2003US-0508225P.

PR 11-MAR-2004; 2004US-0552084P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Chen J, Wu S, Lee N;

XX WPI; 2005-075549/08.

XX N-PSDB; ADW24312.

XX New isolated AdipoR2v1 adiponectin receptor polypeptide and its encoding

PT nucleic acid, useful for diagnosing, preventing and/or treating a

PT disorder related to aberrant adiponectin binding activity and/or

PT expression.

XX Claim 5; SEQ ID NO 165; 469pp; English.

XX The invention relates to a novel isolated AdipoRv (adiponectin receptor

CC splice variant) nucleic acid molecule. Adiponectin

CC (Acrp30/AdipoQ/apM1/GBP28) is the most abundant adipose-specific hormone

CC and acts as an antidiabetic, anti-obese, anti-inflammatory and anti-

CC atherogenic adipokine. The polynucleotide of the invention demonstrates

CC anti-diabetic, antibacterial, anti-arteriosclerotic, cardiovascular-gen.,
 CC cardiant, anti-inflammatory, antilipemic, antibacterial, anorectic,
 CC cytostatic, virucide, antithyroid, metabolic, anabolic and eating-
 CC disorders-gen. activities. The polypeptides and their modulators may be
 CC useful for preventing, treating or ameliorating a disorder selected from
 CC metabolic disorders, inflammatory disorders, cardiovascular disorders,
 CC obesity, diabetes, type I diabetes, type II diabetes, gestational
 CC diabetes, early onset diabetes, insulin resistance, disorders in which
 CC glucose-lowering would be beneficial, disorders in which amelioration of
 CC insulin resistance would be beneficial, disorders in which suppressed FA
 CC influx into liver would be beneficial, disorders in which reduced serum
 CC TG would be beneficial, myocardial infarction, heart failure,
 CC atherosclerosis, arteriosclerosis, disorders associated with aberrant
 CC activity or expression of an adiponectin receptor, disorders associated
 CC with aberrant vascular smooth muscle proliferation, disorders associated
 CC with aberrant foam cell formation, disorders in which inhibition of
 CC macrophage phagocytosis would be beneficial, disorders in which
 CC inhibition of TNF-alpha production would be beneficial, dyslipidemia,
 CC diabetogenic dyslipidemia, mixed dyslipidemia, hypercholesterolemia,
 CC hypertriglyceridemia, hyperlipidemia and anorexia nervosa. The
 CC polypeptides and polynucleotides can also be used in diagnosing,
 CC preventing and treating cancer, and bacterial or viral infectious
 CC disorders. The current sequence is that of a rat Adiporv (adiponectin
 CC receptor splice variant) protein of the invention.

XX Sequence 375 AA;

Query Match 97.9%; Score 1967; DB 9; Length 375;

Best Local Similarity 97.6%; Pred. No. 1.1e-209;

Matches 366; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSHKGSVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKABEEQTCVPQEE 60
 DB 1 MSHKGSVAQNGAPSSNRADTVLAEGLPLEEKGKRAATSPAKABEEQACVPQEE 60
 QY 61 EEEVRVLTLPLOAHAMKMEEFVYKWEGRWRVIPPYDVLDPWLKNDYLLHGHRRPMP 120
 DB 61 EEEVRVLTLPLOAHAMKMEEFVYKWEGRWRVIPPYDVLDPWLKNDYLLHGHRRPMP 120
 QY 121 FRACFKSIPIRHTETGNITWTHLLGFLVFLPLGILTMRLPNMYFMAPLQKVVFGMFFLGA 180
 DB 121 FRACFKSIPIRHTETGNITWTHLLGFLVFLPLGILTMRLPNMYFMAPLQKVVFGMFFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
 QY 241 IVCVLGISAIIVAQWDRFATPKHROTQTRAGVFLGLSLGVVPTMHFTIABGFVKATTVGQM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHROTQTRAGVFLGLSLGVVPTMHFTIABGFVKATTVGQM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPERPPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 DB 301 GWFFLMAVMYITGAGLYAARIPERPPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDSL 375

RESULT 11

ADQ37768

ID ADQ37768 standard; protein; 375 AA.

XX ADQ37768;

AC ADQ37768;

XX 07-OCT-2004 (first entry)

XX Mouse adiponectin receptor AdipoR1 protein SEQ ID NO:6.

XX adiponectin receptor; adiponectin binding; mouse; AdipoR1.

XX Mus musculus.

XX WO2004061108-A1.
 XX 22-JUL-2004.
 PD 12-JUN-2003; 2003WO-JP007515.
 XX 29-DEC-2002; 2002JP-00383738.
 PR (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 PA (NISC) NISSAN CHEM IND LTD.
 XX Kadowaki T, Yamauchi T, Nagai R, Kamon J;
 DR WPI: 2004-543879/52.
 DR N-PSDB; ADQ37767.
 XX New protein having adiponectin binding capacity, useful for screening
 PT ligand, agonist or antagonist with respect to adiponectin receptor.
 XX Claim 1; SEQ ID NO 6; 122pp; Japanese.
 CC The present invention describes an adiponectin receptor protein (I)
 CC having adiponectin binding capacity, and having a sequence of 375, 299,
 CC 375, or 311 amino acids (S1, see SEQ ID NO:2, 4, 6 and 8 (ADQ37764,
 CC ADQ37766, ADQ37768 and ADQ37770)), or a protein which has one or more
 CC amino acid deletion, substitution or addition in (S1). Also described:
 CC (1) a gene (II) encoding (1); (2) a recombinant vector (III) containing
 CC (II); (3) a transformed host (IV) containing (III); (4) an antibody which
 CC reacts with (1) or its fragment; and (5) a kit for screening a ligand, an
 CC agonist or an antagonist with respect to adiponectin receptor, comprising
 CC any one of (I)-(IV). (I) is useful for screening a ligand, an agonist or
 CC an antagonist of adiponectin receptor, which involves contacting the test
 CC substance with (I). The present sequence represents the mouse adiponectin
 CC receptor Adipor1, which is used in the exemplification of the present
 CC invention.

Sequence 375 AA;

Query Match 97.3%; Score 1954; DB 8; Length 375;

Best Local Similarity 96.8%; Pred. No. 3.2e-208;

Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSHKGSVAQNGAPASNRADTVLAEGLPLEEKGKRVIANPPKABEEQTCVPQEE 60
 DB 1 MSHKGSVAQNGAPSGNRADTVLAEGLPLEEKGKRAASSPAKAEEDQACVPQEE 60
 QY 61 EEEVRVLTLPLOAHAMKMEEFVYKWEGRWRVIPPYDVLDPWLKNDYLLHGHRRPMP 120
 DB 61 EEEVRVLTLPLOAHAMKMEEFVYKWEGRWRVIPPYDVLDPWLKNDYLLHGHRRPMP 120
 QY 121 FRACFKSIPIRHTETGNITWTHLLGFLVFLPLGILTMRLPNMYFMAPLQKVVFGMFFLGA 180
 DB 121 FRACFKSIPIRHTETGNITWTHLLGFLVFLPLGILTMRLPNMYFMAPLQKVVFGMFFLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
 QY 241 IVCVLGISAIIVAQWDRFATPKHROTQTRAGVFLGLSLGVVPTMHFTIABGFVKATTVGQM 300
 DB 241 IVCVLGISAIIVAQWDRFATPKHROTQTRAGVFLGLSLGVVPTMHFTIABGFVKATTVGQM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPERPPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 DB 301 GWFFLMAVMYITGAGLYAARIPERPPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQ 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDSL 375

RESULT 12

ADW24160
ID ADW24160 standard; protein; 375 AA.
XX
XX ADW24160;
XX
XX 24-MAR-2005 (first entry)
XX
XX Murine AdipoR1 (adiponectin receptor 1) protein.
DE
XX
XX antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen.;
XX cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;
XX cyostatic; virucide; antithyroid; metabolic; anabolic;
XX eating-disorders-gen.; metabolic disorder; inflammation;
XX cardiovascular disease; nutritional disorder; obesity;
XX insulin dependent diabetes; non-insulin dependent diabetes;
XX inulin resistance; myocardial infarction; cardiac failure;
XX atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;
XX hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;
XX viral infection; AdipoR1; adiponectin receptor 1.
XX
XX Mus musculus.
OS
XX W02005001061-A2.
PN
XX
XX 06-JAN-2005.
PD
XX
XX 24-JUN-2004; 2004WO-US020399.
XX
XX 25-JUN-2003; 2003US-0482324P.
PR
XX 10-JUL-2003; 2003US-0486036P.
PR
XX 04-AUG-2003; 2003US-0492470P.
PR
XX 02-OCT-2003; 2003US-0508225P.
PR
XX 11-MAR-2004; 2004US-0552084P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX
XX Chen J, Wu S, Lee N;
PI
XX WPI; 2005-075549/08.
XX
XX New isolated AdipoR2v1 adiponectin receptor polypeptide and its encoding
PT nucleic acid, useful for diagnosing, preventing and/or treating a
PT disorder related to aberrant adiponectin binding activity and/or
PT expression.
XX
XX Disclosure; SEQ ID NO 8; 469pp; English.
PS
XX
XX The invention relates to a novel isolated AdipoRv (adiponectin receptor
CC splice variant) nucleic acid molecule. Adiponectin
CC (Acrp30/AdipoO/apM1/GPB28) is the most abundant adipose-specific hormone
CC and acts as an antidiabetic, anti-obese, anti-inflammatory and anti-
CC atherogenic adipokine. The polynucleotide of the invention demonstrates
CC antidiabetic, antibacterial, antiarteriosclerotic, cardiovascular-gen.,
CC cardiant, antiinflammatory, antilipemic, anorectic, anorectic,
CC cyostatic, virucide, antithyroid, metabolic, anabolic and eating-
CC disorders-gen. activities. The polypeptides and their modulators may be
CC useful for preventing, treating or ameliorating a disorder selected from
CC metabolic disorders, inflammatory disorders, cardiovascular disorders,
CC obesity, diabetes, type II diabetes, type I diabetes, gestational
CC diabetes, early onset diabetes, insulin resistance, disorders in which
CC glucose-lowering would be beneficial, disorders in which amelioration of
CC insulin resistance would be beneficial, disorders in which suppressed FA
CC influx into liver would be beneficial, disorders in which reduced serum
CC TG would be beneficial, myocardial infarction, heart failure,
CC atherosclerosis, arteriosclerosis, disorders associated with aberrant
CC activity or expression of an adiponectin receptor, disorders associated
CC with aberrant vascular smooth muscle proliferation, disorders associated
CC with aberrant foam cell formation, disorders in which inhibition of
CC macrophage phagocytosis would be beneficial, disorders in which
CC inhibition of TNF-alpha production would be beneficial, dyslipidemia,
CC diabetic dyslipidemia, mixed dyslipidemia, hypercholesterolemia,
CC hypertriglyceridemia, hyperlipidemia and anorexia nervosa. The
CC polypeptides and polynucleotides can also be used in diagnosing,

CC preventing and treating cancer, and bacterial or viral infectious
CC disorders. The current sequence is that of a murine AdipoR (adiponectin
CC receptor) protein of the invention.
XX
XX Sequence 375 AA;
SQ
Query Match 97.3%; Score 1954; DB 9; Length 375;
Best Local Similarity 96.8%; Pred. No. 3.2e-208; Indels 0; Gaps 0;
Matches 363; Conservative 5; Mismatches 7;
QY 1 MSHKSGSVVAAQNGAPASNRREADTVLAEGLPLEEKGRVIANPPKAESEQTCVPVQEE 60
DB 1 MSHKSGSAGAQNGAPSGNREADTVLAEGLPLEEKGRVIANPPKAESEQTCVPVQEE 60
QY 61 EBEVRVLTPLQAHAMEKMEBFVYKWEGRVPIPYDVLVDWLDNDYLLHGHRRPMP 120
DB 61 EBEVRVLTPLQAHAMEKMEBFVYKWEGRVPIPYDVLVDWLDNDYLLHGHRRPMP 120
QY 121 FRACPKSIFRIHTETGNIWTHLLGFVLFPLGLTLMRLPNMYFMAPLQEKVFGMEFLGA 180
DB 121 FRACPKSIFRIHTETGNIWTHLLGFVLFPLGLTLMRLPNMYFMAPLQEKVFGMEFLGA 180
QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMYYSFYCSPPRLIYLS 240
DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMYYSFYCSPPRLIYLS 240
QY 241 IVCVLGISAIIVAQWDRFATPKHROTQTRAGVFLGLSLGVVPTMHTIAGFVKATTVGOM 300
DB 241 IVCVLGISAIIVAQWDRFATPKHROTQTRAGVFLGLSLGVVPTMHTIAGFVKATTVGOM 300
QY 301 GWFFLMAVMYITGAGLYAARIIPERPPGKFDIWFQSHOIFHVLVVAFAFVHFYGVSNLQE 360
DB 301 GWFFLMAVMYITGAGLYAARIIPERPPGKFDIWFQSHOIFHVLVVAFAFVHFYGVSNLQE 360
QY 361 FRYGLEGGCTDITLL 375
DB 361 FRYGLEGGCTDITLL 375
RESULT 13
AAU30936
ID AAU30936 standard; protein; 387 AA.
XX
XX AAU30936;
XX
XX 18-DEC-2001 (first entry)
XX
XX Novel human secreted protein #1427.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX W0200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSB-) HYSB INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX

PS Claim 20; Page 379; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising the

CC nucleic acids encoding the polypeptides and cells genetically engineered

CC to express them are also useful for producing the proteins. The proteins

CC are useful in genetic vaccination, testing and therapy, and can be used

CC as nutritional supplements. They may be used to increase stem cell

CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon

CC and/or nerve tissue growth or regeneration; immune suppression and/or

CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

CC AAU29510-AAU33304 represent the amino acid sequences of novel human

CC secreted proteins of the invention

XX Sequence 387 AA;

SQ

Query Match 84.4%; Score 1696; DB 4; Length 387;

Best Local Similarity 89.1%; Pred. No. 1.8e-179;

Matches 335; Conservative 5; Mismatches 28; Indels 8; Gaps 8;

QY 1 MSHKGSVAQNGAPASNRADTVELAGLPLEEKGKRVIANPPKAEETQCPVQEE 60

DB 11 MSHKGSVAQNGAPASNRADTVELAGLPLEEKGKRVIANPPKAEETQCPVQEE 70

QY 61 EEEVRVLTPLQAHAMEKMEFVYKWEGRWRVPIYDVLDPWLKONDYLLGHRPPMPS 120

DB 71 EEEVRVLTPLQAHAMEKMEFVYKWEGRWRVPIYDVLDPWLKONDYLLGHRPPMPS 130

QY 121 FRACPKSIFRIHTETGNITWHL-LGFVFLFLGLTLMRLPNMYFMAPLQE-KVFGMPPL 178

DB 131 FRACPKSIFRIHTETGNITWHLALGFVFLFLGLTLMRLPNMYFMAPLQEKVKVFGMPPL 190

QY 179 GAVLCLSFSLHFTVYCHSEKVSRTFSKLD-VSGIALLTWSG-FVPLWYVFCSPQPL 236

DB 191 GAVLCLSFSLHFTVYCHGFPVSTFPQRELFGLLLNWGLWSGLYYSFCSPQPL 250

QY 237 IYLSIVCVLGISAIIVQWDRFATPKHRTAGVFLGLGLSGVVPVPMHTTIA-EGFVKAT 295

DB 251 IYLSIVCVLGISAIIVQWDRFATPKHRTAGVFLGLGLSGVVPVPMHTTNRWALSAT 310

QY 296 TVGQMGWFFLMAVWYITG-AGLYAARIPERFFPGKFDIWFQSHQIPHVLVWAAAFVHYG 354

DB 311 TVGQMGWFFLMAVWYITGLAFNAARIPERFFPGKFDIWFQSHQIPHVLVWAAAFVHYG 370

QY 355 -VSNLQEPFY-GLGG 368

DB 371 SVSNLQEPFLTGLEGG 386

RESULT 14

ID ADW24251

XX ADW24251 standard; protein; 381 AA.

AC ADW24251;

XX

XX 24-MAR-2005 (first entry)

XX

DE Human AdipoR3v1 (adiponectin receptor 3 splice variant 1) protein.

XX

KW antidiabetic; antibacterial; antiarteriosclerotic; cardiovascular-gen.;

KW cardiant; antiinflammatory; antilipemic; antibacterial; anorectic;

KW cytotatic; virucide; antithyroid; metabolic; anabolic;

KW cating-disorders-gen.; metabolic disorder; inflammation;

KW cardiovascular disease; nutritional disorder; obesity;

KW insulin dependent diabetes; non-insulin dependent diabetes;

KW insulin resistance; myocardial infarction; cardiac failure;

KW atherosclerosis; arteriosclerosis; dyslipidemia; hypercholesterolemia;

KW

KW hyperlipidemia; anorexia nervosa; cancer; neoplasm; bacterial infection;

KW viral infection; AdipoR3v1; adiponectin receptor 3.

XX Homo sapiens.

OS WO2005001061-A2.

FN 06-JAN-2005.

PD 24-JUN-2004; 2004WO-US020399.

XX 25-JUN-2003; 2003US-0482324P.

XX 10-JUL-2003; 2003US-0486036P.

PR 04-AUG-2003; 2003US-0492470P.

PR 02-OCT-2003; 2003US-0508225P.

PR 11-MAR-2004; 2004US-0552084P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Chen J, Wu S, Lee N;

XX WPI: 2005-075549/08.

XX N-PSDB; ADW24250.

DR

DR New isolated AdipoR2v1 adiponectin receptor polypeptide and its encoding

PT nucleic acid, useful for diagnosing, preventing and/or treating a

PT disorder related to aberrant adiponectin binding activity and/or

PT expression.

PS Claim 5; SEQ ID NO 102; 469pp; English.

XX The invention relates to a novel isolated AdipoRv (adiponectin receptor

CC splice variant) nucleic acid molecule. Adiponectin

CC (Acrp30/Adipoq/apM1/GBP28) is the most abundant adipose-specific hormone

CC and acts as an antidiabetic, anti-obese, anti-inflammatory and anti-

CC atherogenic adipokine. The polynucleotide of the invention demonstrates

CC antidiabetic, antibacterial, antiarteriosclerotic, cardiovascular-gen.,

CC cardiant, antiinflammatory, antilipemic, antibacterial, anorectic,

CC cytotatic, virucide, antithyroid, metabolic, anabolic, and eating-

CC disorders-gen activities. The polypeptides and their modulators may be

CC useful for preventing, treating or ameliorating a disorder selected from

CC metabolic disorders, inflammatory disorders, cardiovascular disorders,

CC obesity, diabetes, type II diabetes, type II diabetes, gestational

CC diabetes, early onset diabetes, insulin resistance, disorders in which

CC glucose-lowering would be beneficial, disorders in which amelioration of

CC insulin resistance would be beneficial, disorders in which suppressed FA

CC influx into liver would be beneficial, disorders in which reduced serum

CC TG would be beneficial, myocardial infarction, heart failure,

CC atherosclerosis, arteriosclerosis, disorders associated with aberrant

CC activity or expression of an adiponectin receptor, disorders associated

CC with aberrant vascular smooth muscle proliferation, disorders associated

CC with aberrant foam cell formation, disorders in which inhibition of

CC macrophage phagocytosis would be beneficial, disorders in which

CC inhibition of TNF-alpha production would be beneficial, dyslipidemia,

CC diabetic dyslipidemia, mixed dyslipidemia, hypercholesterolemia,

CC hypertriglyceridemia, hyperlipidemia and anorexia nervosa. The

CC polypeptides and polynucleotides can also be used in diagnosing,

CC preventing and treating cancer, and bacterial or viral infectious

CC disorders. The current sequence is that of a human AdipoRv (adiponectin

CC receptor splice variant) protein of the invention.

XX Sequence 381 AA;

SQ

Query Match 76.1%; Score 1529; DB 9; Length 381;

Best Local Similarity 79.9%; Pred. No. 7.2e-161;

Matches 306; Conservative 15; Mismatches 52; Indels 10; Gaps 4;

QY 1 MSHKGSVAQNGAPASNRADTVELA--ELGPLLEEKGKRVIANPPKAEETQCPVQ 58

DB 1 MSHKGSVAQNGAPASNRADTVELA--ELGPLLEEKGKRVIANPPKAEETQCPVQ 59

QY 59 EEEVRVLTPLQAHAMEKMEFVYKWEGRWRVPIYDVLDPWLK-----DNDYLLH 112

Db 60 EBEERWVLTPLQAHHTMEKMEFVYKLTSCCH-HQVDGLPDWLKONDCLQNDCLLY 118
QY 113 GHRPPMPSPFRACFKSIFRIHTETGNIWTHLLGFLFLGILTMRLPNMYFNAPLOEKVV 172
Db 119 GHRQPMSSFWACFKSIFYIHTETGSSRTHLLGFLFLGILTMRLPNMYFTAPLQEKVI 178
QY 173 FGMFFLGAVLCFSFWLFTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYPCSP 232
Db 179 WRIFLLGAVLSFSFWLFTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYPCSP 238
QY 233 QPRLIYLSIVCVLIGISAIIVADQDRATPKHROTGRAGVFLGSLGVPMTHTIAEGFV 292
Db 239 QPRLIYFSIYVIGISAIIVDQDRFVTPKHROTGRAGVFLGSLGIVPTMTHTIAEGFV 298
QY 293 KATTVQMGWFFFLMVMYITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHF 352
Db 299 KATTVQMGWFFFLVAVMYITRAGLYAALIPERFPFGKLDIWFQSQIFHVLVMTVAFVHF 358
QY 353 YGVSNLOEFYRLEGCGTDTLL 375
Db 359 CGVSNLQEFHYSGREGDCTDLSL 381

RESULT 15

ADR09023
ID ADR09023 standard; protein; 386 AA.

AC ADR09023;

XX 04-NOV-2004 (first entry)

DE Human protein useful for treating neurological disease Seq 2529.

XX human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
KW tranquiliser.

XX Homo sapiens.

XX EP1447413-A2.

XX 18-AUG-2004.

XX 12-FEB-2004; 2004EP-00003145.

XX 14-FEB-2003; 2003JP-00102207.

XX 09-MAY-2003; 2003JP-00131452.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;

PI Wakamatsu A, Ishii S, Nagai K, Irie R;

XX WPI; 2004-583265/57.

XX N-PSDB; ADR07067.

XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX Claim 1; SEQ ID NO 2529; 2686pp; English.

XX This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in

CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cyostatic and tranquiliser activities. This polypeptide is a protein
CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.

XX Sequence 386 AA;

QY Query Match 69.9%; Score 1403.5; DB 8; Length 386;

XX Best Local Similarity 70.7%; Pred. No. 78-147; Indels 7; Gaps 3;

XX Matches 260; Conservative 43; Mismatches 58; Indels 7; Gaps 3;

QY 11 QCGAPASNREADTVELAELGLPBLEKGRKRVIANPPK---ABEEQTCVPVQBEERVRVL 67

Db 23 KGHQDGTGRGNDSDHQDLEFLEAS---VLSSHKKSSSEHEYSDEAPQDEGFMGMS 79

QY 68 TLPLOAHAMEROMEFVYKVGWRVPIPYDVLPDWLKONDYLLHGRHPMPSPFRACFKS 127

Db 80 PL-LQAHAMEROMEFVYKVGWRVPIPHDVLPDWLKONDYLLHGRHPMPSPFRACFKS 138

QY 128 IFRIHTETGNIWTHLLGFLFLGILTMRLPNMYFNAPLOEKVYFGMFFLGAVLCLSFS 187

Db 139 IFRIHTETGNIWTHLLGCVFFLCGLGIFYMFRENISFVAELQEKVYFGMFFLGAVLCLSFS 198

QY 188 WLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYPCSPOPRIYLSIVCVLGI 247

Db 199 WLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYPCSNPQPCFIYLVICVLGI 258

QY 248 SAIIVAQWDRFATPKHROTGRAGVFLGSLGSGVVPMTHTIAEGFVKAATTVQMGWFFLMA 307

Db 259 AAIIVSQWDMFATPQYRGVRAAGVFLGSLGSGIIPTLHYVISBGFLKAATIGQIGWMLMA 318

QY 308 VMIITGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHFYGVSNLOEFYRLEG 367

Db 319 SLVITGAALYAARIPERFPFGKCDIWFHSHQLFHFVAVAGAFVHFHGVSNLOEFYRLEMIG 378

QY 368 GCTDITLL 375

Db 379 GCSEEDAL 386

Search completed: April 19, 2006, 13:57:15

Job time : 219.657 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2006, 14:18:45 ; Search time 127.967 Seconds
(without alignments)
1224.422 Million cell updates/sec

Title: US-10-799-943-2
Perfect score: 2009
Sequence: 1 MSHKGSVVAQNGAPASNR.....SNLQFRYGLGGCTDDTL 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2009	100.0	375	3	US-09-965-529-5
2	2009	100.0	375	3	US-09-969-680A-5
3	2009	100.0	375	4	US-10-264-237-2289
4	2009	100.0	375	5	US-10-799-943-2
5	2009	100.0	375	5	US-10-874-923-7
6	2009	100.0	375	6	US-11-048-692-5
7	1967	97.9	375	5	US-10-874-923-165
8	1954	97.3	375	5	US-10-799-943-6
9	1954	97.3	375	5	US-10-874-923-8
10	1529	76.1	381	5	US-10-874-923-102
11	1403.5	69.9	386	5	US-10-874-923-2
12	1391.5	68.3	386	5	US-10-874-923-4
13	1378.5	68.6	311	5	US-10-799-943-167
14	1378	68.6	311	5	US-10-799-943-8
15	1378	68.6	311	5	US-10-874-923-10
16	1376	68.5	421	5	US-10-874-923-104
17	1347	67.0	299	5	US-10-799-943-4
18	1345	66.9	299	5	US-10-874-923-9
19	1344	66.9	299	4	US-10-236-352-42
20	1075	53.5	201	3	US-09-948-783-131
21	1075	53.5	202	3	US-09-892-877-129
22	1052.5	52.4	288	5	US-10-874-923-6
23	1016.5	50.6	444	6	US-11-097-143-11043
24	1001.5	49.9	322	6	US-11-097-143-25536
25	674	33.5	228	4	US-10-264-237-2158
26	662	33.0	238	4	US-10-080-334-124
27	583	29.0	286	4	US-10-004-378A-134

28	501	24.9	360	4	US-10-424-599-252700	Sequence 252700,
29	499	24.8	384	4	US-10-425-114-51693	Sequence 51693, A
30	498.5	24.8	351	4	US-10-425-115-243901	Sequence 243901,
31	482.5	24.0	435	4	US-10-425-114-56352	Sequence 56352, A
32	482.5	24.0	438	4	US-10-425-114-73037	Sequence 73037, A
33	482	24.0	379	4	US-10-437-963-187447	Sequence 187447,
34	481	23.9	380	5	US-10-739-930-9197	Sequence 9197, Ap
35	477	23.7	345	5	US-10-739-930-7323	Sequence 7323, Ap
36	475.5	23.7	380	4	US-10-425-115-330861	Sequence 330861,
37	475	23.6	402	4	US-10-425-115-330861	Sequence 127004,
38	475	23.6	430	4	US-10-437-963-137004	Sequence 63314, A
39	475	23.6	440	4	US-10-425-114-63314	Sequence 8435, Ap
40	471.5	23.5	348	5	US-10-739-930-8435	Sequence 7324, Ap
41	471.5	23.5	380	5	US-10-739-930-7324	Sequence 159720,
42	465	23.1	376	4	US-10-437-963-159720	Sequence 182445,
43	461.5	23.0	370	4	US-10-437-963-182445	Sequence 32, Appl
44	397.5	19.8	311	5	US-10-483-512-32	Sequence 178844,
45	372	18.5	210	4	US-10-424-599-178844	

ALIGNMENTS

RESULT 1

US-09-965-529-5

; Sequence 5, Application US/09965529

; Publication No. US20020182671A1

; GENERAL INFORMATION:

; APPLICANT: LAL, Preeti

; APPLICANT: YUE, Henry

; APPLICANT: TANG, Y. Tom

; APPLICANT: BANDMAN, Olga

; APPLICANT: BURFORD, Neil

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: LU, Dyrung Aina M.

; APPLICANT: PATTERSON, Chandra

; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS

; FILE REFERENCE: PF-0731 USA

; CURRENT APPLICATION NUMBER: US/09/965,529

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 60/149,641; 60/164,203; PCT/US00/22315

; PRIOR FILING DATE: 1999-08-17; 1999-11-09; 2000-08-14

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program

; SEQ ID NO 5

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20020182671A1 2071941CD1

US-09-965-529-5

Query Match 100.0%; Score 2009; DB 3; Length 375;

Best Local Similarity 100.0%; Pred. No. 1.5e-182;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSHKGSVVAQNGAPASNR	ADTVLAEI	GPLLEKGRVIANPPKAE	EEQTCVPQEE	60
Db	1	MSHKGSVVAQNGAPASNR	ADTVLAEI	GPLLEKGRVIANPPKAE	EEQTCVPQEE	60
Qy	61	EEVRVLTLPLOAHAMKME	EFVYKVG	GRWVPI	PDVLPDL	KNDYLLHGRHPMPS 120
Db	61	EEVRVLTLPLOAHAMKME	EFVYKVG	GRWVPI	PDVLPDL	KNDYLLHGRHPMPS 120
Qy	121	FRACFSIFRIHTETGN	WTHLLG	FLVFL	PLGLTLM	RPNMYMAPLOEKVFGMFLGA 180
Db	121	FRACFSIFRIHTETGN	WTHLLG	FLVFL	PLGLTLM	RPNMYMAPLOEKVFGMFLGA 180
Qy	181	VLCLFSWLPHTYVCH	SEKSVRT	FSKLDY	SGIALL	MGSPVPLWLYSFYCSPOPRLIYLS 240
Db	181	VLCLFSWLPHTYVCH	SEKSVRT	FSKLDY	SGIALL	MGSPVPLWLYSFYCSPOPRLIYLS 240

;; CURRENT FILING DATE: 2004-03-11
;; PRIOR APPLICATION NUMBER: PCT/JP03/07515
;; PRIOR FILING DATE: 2003-06-12
;; PRIOR APPLICATION NUMBER: JP 2002-383738
;; PRIOR FILING DATE: 2002-12-29
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 375
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-799-943-2

Query Match 100.0%; Score 2009; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-182;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRKRVIANPPKAESEOTCPVPOEE 60
DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRKRVIANPPKAESEOTCPVPOEE 60
QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLPDWLKNDYLLHGHRRPMP 120
DB 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLPDWLKNDYLLHGHRRPMP 120
QY 121 FRACFKSIIRIHTETGNIWTHLLGFVFLPLGILTMLRPNMYPMAFLOEKVFGMFFLGA 180
DB 121 FRACFKSIIRIHTETGNIWTHLLGFVFLPLGILTMLRPNMYPMAFLOEKVFGMFFLGA 180
QY 181 VLCLSFSLFWHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
DB 181 VLCLSFSLFWHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
QY 241 IVCVLGISAIIVAQMDRFATPKHROTQTRAGVFLGLSGVVPVTHFTIABGFVKATTVGOM 300
DB 241 IVCVLGISAIIVAQMDRFATPKHROTQTRAGVFLGLSGVVPVTHFTIABGFVKATTVGOM 300
QY 301 GWFFLMAVMIITGAGLYAARIPIRPFPGKEDIWFQSHQIHFVLVVAAPVHFYGVSNLQ 360
DB 301 GWFFLMAVMIITGAGLYAARIPIRPFPGKEDIWFQSHQIHFVLVVAAPVHFYGVSNLQ 360
QY 361 FRYGLEGGCTDDTL 375
DB 361 FRYGLEGGCTDDTL 375

RESULT 5
US-10-874-923-7
;; Sequence 7, Application US/10874923
;; Publication No. US2005032166A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
;; FILE REFERENCE: D0338 NP
;; CURRENT APPLICATION NUMBER: US/10/874,923
;; CURRENT FILING DATE: 2004-06-23
;; PRIOR APPLICATION NUMBER: U.S. 60/482,324
;; PRIOR FILING DATE: 2003-06-25
;; PRIOR APPLICATION NUMBER: U.S. 60/486,036
;; PRIOR FILING DATE: 2003-07-10
;; PRIOR APPLICATION NUMBER: U.S. 60/492,470
;; PRIOR FILING DATE: 2003-08-04
;; PRIOR APPLICATION NUMBER: U.S. 60/508,225
;; PRIOR FILING DATE: 2003-10-02
;; PRIOR APPLICATION NUMBER: U.S. 60/552,084
;; PRIOR FILING DATE: 2004-03-11
;; NUMBER OF SEQ ID NOS: 248
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 7
;; LENGTH: 375
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-874-923-7

Query Match 100.0%; Score 2009; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-182;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRKRVIANPPKAESEOTCPVPOEE 60
DB 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRKRVIANPPKAESEOTCPVPOEE 60
QY 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLPDWLKNDYLLHGHRRPMP 120
DB 61 EEEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLPDWLKNDYLLHGHRRPMP 120
QY 121 FRACFKSIIRIHTETGNIWTHLLGFVFLPLGILTMLRPNMYPMAFLOEKVFGMFFLGA 180
DB 121 FRACFKSIIRIHTETGNIWTHLLGFVFLPLGILTMLRPNMYPMAFLOEKVFGMFFLGA 180
QY 181 VLCLSFSLFWHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
DB 181 VLCLSFSLFWHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYLS 240
QY 241 IVCVLGISAIIVAQMDRFATPKHROTQTRAGVFLGLSGVVPVTHFTIABGFVKATTVGOM 300
DB 241 IVCVLGISAIIVAQMDRFATPKHROTQTRAGVFLGLSGVVPVTHFTIABGFVKATTVGOM 300
QY 301 GWFFLMAVMIITGAGLYAARIPIRPFPGKEDIWFQSHQIHFVLVVAAPVHFYGVSNLQ 360
DB 301 GWFFLMAVMIITGAGLYAARIPIRPFPGKEDIWFQSHQIHFVLVVAAPVHFYGVSNLQ 360
QY 361 FRYGLEGGCTDDTL 375
DB 361 FRYGLEGGCTDDTL 375

RESULT 6
US-11-048-692-5
;; Sequence 5, Application US/11048692
;; Publication No. US20050123990A1
;; GENERAL INFORMATION:
;; APPLICANT: LAL, Preeti; YUE, Henry
;; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
;; APPLICANT: BURFORD, Neil; AZIMZAI, Valda
;; APPLICANT: BAUGHN, Mariah R.; LU, Dyoung Aina M.
;; APPLICANT: PATTERSON, Chandra
;; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
;; FILE REFERENCE: PF-0731-1 USA
;; CURRENT APPLICATION NUMBER: US/11/048,692
;; CURRENT FILING DATE: 2005-02-02
;; PRIOR APPLICATION NUMBER: US/09/969,680
;; PRIOR FILING DATE: 2001-10-02
;; PRIOR APPLICATION NUMBER: US00/22315
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/149,641
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/164,203
;; PRIOR FILING DATE: 1999-11-09
;; NUMBER OF SEQ ID NOS: 74
;; SOFTWARE: PERL Program
;; SEQ ID NO 5
;; LENGTH: 375
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No: 2071941CD1
US-11-048-692-5

Query Match 100.0%; Score 2009; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.5e-182;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRKRVIANPPKAESEOTCPVPOEE 60

```
Db 1 MSHKGSVVAQNGAPASNREADTVLAEGLPDLLEKGRVIANPPKAEBEQTCVPQBE 60
Qy 61 EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLDPWLKNDYLLHGRPPMPS 120
Db 61 EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLDPWLKNDYLLHGRPPMPS 120
Qy 121 FRACFKSIFRIHTETGNIWTHLLGFVFLFLGLGILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Db 121 FRACFKSIFRIHTETGNIWTHLLGFVFLFLGLGILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Qy 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVFWLYYSPYCSQPRLIYLS 240
Db 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVFWLYYSPYCSQPRLIYLS 240
Qy 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGOM 300
Db 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGOM 300
Qy 301 GWFFLMAVMYITGAGLYAARIPEFPFGKFDIWFQSHQIFHVLVVAAAFVHFYGVSNLQOE 360
Db 301 GWFFLMAVMYITGAGLYAARIPEFPFGKFDIWFQSHQIFHVLVVAAAFVHFYGVSNLQOE 360
Qy 361 FRYGLEGGCTDDTL 375
Db 361 FRYGLEGGCTDDTL 375

RESULT 7
US-10-874-923-165
; Sequence 165, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; PRIOR FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-874-923-165

Query Match 97.9%; Score 1967; DB 5; Length 375;
Best Local Similarity 97.6%; Pred. No. 1.5e-178;
Matches 366; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MSHKGSVVAQNGAPASNREADTVLAEGLPDLLEKGRVIANPPKAEBEQTCVPQBE 60
Db 1 MSHKGSVVAQNGAPASNREADTVLAEGLPDLLEKGRVIANPPKAEBEQTCVPQBE 60
Qy 61 EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLDPWLKNDYLLHGRPPMPS 120
Db 61 EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLDPWLKNDYLLHGRPPMPS 120
Qy 121 FRACFKSIFRIHTETGNIWTHLLGFVFLFLGLGILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Db 121 FRACFKSIFRIHTETGNIWTHLLGFVFLFLGLGILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Qy 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVFWLYYSPYCSQPRLIYLS 240
Db 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVFWLYYSPYCSQPRLIYLS 240
```

```
Db 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVFWLYYSPYCSQPRLIYLS 240
Qy 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGOM 300
Db 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGOM 300
Qy 301 GWFFLMAVMYITGAGLYAARIPEFPFGKFDIWFQSHQIFHVLVVAAAFVHFYGVSNLQOE 360
Db 301 GWFFLMAVMYITGAGLYAARIPEFPFGKFDIWFQSHQIFHVLVVAAAFVHFYGVSNLQOE 360
Qy 361 FRYGLEGGCTDDTL 375
Db 361 FRYGLEGGCTDDSL 375

RESULT 8
US-10-799-943-6
; Sequence 6, Application US/10799943
; Publication No. US20040241802A1
; GENERAL INFORMATION:
; APPLICANT: KADOWAKI, Takashi
; APPLICANT: YAMAUCHI, Toshimasa
; APPLICANT: NAGAI, Ryozi
; APPLICANT: KAMON, Jyunji
; TITLE OF INVENTION: ADIPONECTIN RECEPTOR AND GENE ENCODING
; FILE REFERENCE: ARV-002
; CURRENT APPLICATION NUMBER: US/10/799,943
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: PCT/JF03/07515
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002-383738
; PRIOR FILING DATE: 2002-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-799-943-6

Query Match 97.3%; Score 1954; DB 5; Length 375;
Best Local Similarity 96.8%; Pred. No. 2.7e-177;
Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MSHKGSVVAQNGAPASNREADTVLAEGLPDLLEKGRVIANPPKAEBEQTCVPQBE 60
Db 1 MSHKGSVVAQNGAPASNREADTVLAEGLPDLLEKGRVIANPPKAEBEQTCVPQBE 60
Qy 61 EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLDPWLKNDYLLHGRPPMPS 120
Db 61 EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVVPYDVLDPWLKNDYLLHGRPPMPS 120
Qy 121 FRACFKSIFRIHTETGNIWTHLLGFVFLFLGLGILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Db 121 FRACFKSIFRIHTETGNIWTHLLGFVFLFLGLGILTMLRPNMYFMAPLQEKVVFQGMFFLGA 180
Qy 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVFWLYYSPYCSQPRLIYLS 240
Db 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMGSFVFWLYYSPYCSQPRLIYLS 240
Qy 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGOM 300
Db 241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTTIAEGFVKATTVGOM 300
Qy 301 GWFFLMAVMYITGAGLYAARIPEFPFGKFDIWFQSHQIFHVLVVAAAFVHFYGVSNLQOE 360
Db 301 GWFFLMAVMYITGAGLYAARIPEFPFGKFDIWFQSHQIFHVLVVAAAFVHFYGVSNLQOE 360
Qy 361 FRYGLEGGCTDDTL 375
Db 361 FRYGLEGGCTDDSL 375
```



```
RESULT 9
US-10-874-923-8
; Sequence 8, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-874-923-8

Query Match          97.3%; Score 1954; DB 5; Length 375;
Best Local Similarity 96.8%; Pred. No. 2.7e-177;
Matches 363; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 MSHKGSVVAQNGAPASNREADTVELAEGLPILLEKGRKVIANPPKABEEQTCVPQOE 60
Db      1 MSHKGSAGAGNGAPSGNREADTVELAEGLPILLEKGRKRAASPAKAEEDQACPQOE 60

QY      61 EEEVRVLTLPLOAHAMEKEEFYKVGWRVRVPIYDVLDPDLKNDYLLHGRPPMP 120
Db      61 EEEVRVLTLPLOAHAMEKEEFYKVGWRVRVPIYDVLDPDLKNDYLLHGRPPMP 120

QY      121 FRACFKSIFRIHTETGNIWTHLLGFVLFLFLGILTMLRPNMYFMAPLOEKVFGMPFLGA 180
Db      121 FRACFKSIFRIHTETGNIWTHLLGFVLFLFLGILTMLRPNMYFMAPLOEKVFGMPFLGA 180

QY      181 VLCLSPFLFHTYVCHSEKVSRTFSKLDYSGIALLIMGSFVPMLYSYFCSPQRLIYLS 240
Db      181 VLCLSPFLFHTYVCHSEKVSRTFSKLDYSGIALLIMGSFVPMLYSYFCSPQRLIYLS 240

QY      241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLGLSGVVPTMHTTIAEGFVKATTVGOM 300
Db      241 IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLGLSGVVPTMHTTIAEGFVKATTVGOM 300

QY      301 GWFFLMAVYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVWAAAFVHFYGVSNLQ 360
Db      301 GWFFLMAVYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVWAAAFVHFYGVSNLQ 360

QY      361 FRYLEGCGCTDDTL 375
Db      361 FRYLEGCGCTDDSL 375

RESULT 10
US-10-874-923-102
; Sequence 102, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
```

```
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 102
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-874-923-102

Query Match          76.1%; Score 1529; DB 5; Length 381;
Best Local Similarity 79.9%; Pred. No. 8.8e-137;
Matches 306; Conservative 15; Mismatches 52; Indels 10; Gaps 4;

QY      1 MSHKGSVVAQNGAPASNREADTVELA--ELGPLLEKGRKVIANPPKABEEQTCVPQ 58
Db      1 MSHKGSVVAR-NGAPASNRETDVLAESLSPLLEKGRKVIANPPKABEEQTCVPQ 59

QY      59 EEEVRVLTLPLOAHAMEKEEFYKVGWRVRVPIYDVLDPDLK-----DNDYLLH 112
Db      60 EEEVRVLTLPLOAHHTMEKEEFYKLTQSCCH-HQYDGLPDLKONDCLQDNDCLLY 118

QY      113 GHRPMPSPRACFKSIFRIHTETGNIWTHLLGFVLFLFLGILTMLRPNMYFMAPLOEKVV 172
Db      119 GHRQPMSSFWACFKSIFYIHTETGSRTHLLGFVLFLFLGILTMLRPNMYFMAPLOEKV 178

QY      173 FGMFFLGAIVCLSPFLFHTYVCHSEKVSRTFSKLDYSGIALLIMGSFVPMLYSYFCSP 232
Db      179 WRIFLGLAVLSLSPFLFHTYVCHSEKVSRTFSKLDYSGIALLIMGSFVPMLYSYFCSP 238

QY      233 QRLIYLSIVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLGLSGVVPTMHTTIAEGFV 292
Db      239 QRLIYFSIIYVVLGISAIIVDQWDRFVTPKHQTRAGVLLGLGLSGIVPTMHTTIAEGFV 298

QY      293 KATTVGQMGFFLMAVYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVWAAAFVHF 352
Db      299 KATTVGQMGFFLMAVYITRAGLYAALIPERFFPGKLDIWFQSQQIFHVLVWTVAFVHF 358

QY      353 YGVSNLQEFYRGLGCGCTDDTL 375
Db      359 CGVSNLQEFYHSGEGCTDDSL 381

RESULT 11
US-10-874-923-2
; Sequence 2, Application US/10874923
; Publication No. US20050032166A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
; FILE REFERENCE: D0338 NP
; CURRENT APPLICATION NUMBER: US/10/874,923
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: U.S. 60/482,324
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: U.S. 60/486,036
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: U.S. 60/492,470
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: U.S. 60/508,225
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: U.S. 60/552,084
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
```


QY 243 CVLGISAIIVAQWDRFATPKHRTQAGVFLGLGLSGVPTMHFTIAEGFVKATTVQMGW 302
 Db 254 CVLGIAAIIVSQWDMFATPQYGRAGVFLGLGLSGIIPTHLVISEGFLKAATIRQIGW 313
 QY 303 FFLMAVYITGAGLYAARIPIPERFPKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQEF 362
 Db 314 LMLMASLYITGAALYAARIPIPERFPKCDIWFHSHQIFHIFVVGAGFVHFHGVSNLQEF 373
 QY 363 YGLEGGCTDITLL 375
 Db 374 FMIGGGCTEKDAL 386

RESULT 14

US-10-799-943-8
 ; Sequence 8, Application US/10799943
 ; Publication No. US20040241802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KADOWAKI, Takashi
 ; APPLICANT: YAMAUCHI, Toshimasa
 ; APPLICANT: NAGAI, Ryozo
 ; APPLICANT: KAWON, Jyunji
 ; TITLE OF INVENTION: ADIPONECTIN RECEPTOR AND GENE ENCODING
 ; FILE REFERENCE: ARV-002
 ; CURRENT APPLICATION NUMBER: US/10/799,943
 ; CURRENT FILING DATE: 2004-03-11
 ; PRIOR APPLICATION NUMBER: PCT/JP03/07515
 ; PRIOR FILING DATE: 2003-06-12
 ; PRIOR APPLICATION NUMBER: JP 2002-383738
 ; PRIOR FILING DATE: 2002-12-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-799-943-8

Query Match 68.6%; Score 1378; DB 5; Length 311;
 Best Local Similarity 80.0%; Pred. No. 1.6e-122;
 Matches 244; Conservative 31; Mismatches 30; Indels 0; Gaps 0;
 QY 71 LQAHAMERKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPSPFRACFKSIFR 130
 Db 7 LQAHAMERKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPSPFRACFKSIFR 66
 QY 131 IHTETGNIWTHLLGFLVFLFLGILTLMLRPNMYFMAPLQEKVFGMFFLGAVALCLSPSWLF 190
 Db 67 IHTETGNIWTHLLGCVFFLCIGIFYMFRPNISFVAPLQEKVFGMFFLGAVALCLSPSWLF 126
 QY 191 HTVYCHSEKVSRTSKLDYSGIALLIMSGFVPMWLYSYFYCSQPRLIYLSIVCVLGISAI 250
 Db 127 HTVYCHSEGVSRFLSKLDYSGIALLIMSGFVPMWLYSYFYCNPCFTYILIVICVLGIAAI 186
 QY 251 IVAQWDRFATPKHRTQAGVFLGLGLSGVPTMHFTIAEGFVKATTVQMGWFFLMAVY 310
 Db 187 IVSQWDMFATPQYGRAGVFLGLGLSGIIPTHLVISEGFLKAATIRQIGWMLMASLY 246
 QY 311 ITGAGLYAARIPIPERFPKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQEFRYGLEGGCT 370
 Db 247 ITGAALYAARIPIPERFPKCDIWFHSHQIFHIFVVGAGFVHFHGVSNLQEFRFMIGGCT 306
 QY 371 DITLL 375
 Db 307 EEDAL 311

RESULT 15

US-10-874-923-10
 ; Sequence 10, Application US/10874923
 ; Publication No. US20050032166A1

; GENERAL INFORMATION:
 ; APPLICANT: Briscot-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ADIPONECTIN RECEPTOR VARIANTS
 ; FILE REFERENCE: D0338 NP
 ; CURRENT APPLICATION NUMBER: US/10/874,923
 ; CURRENT FILING DATE: 2004-06-23
 ; PRIOR APPLICATION NUMBER: U.S. 60/482,324
 ; PRIOR FILING DATE: 2003-06-25
 ; PRIOR APPLICATION NUMBER: U.S. 60/486,036
 ; PRIOR FILING DATE: 2003-07-10
 ; PRIOR APPLICATION NUMBER: U.S. 60/492,470
 ; PRIOR FILING DATE: 2003-08-04
 ; PRIOR APPLICATION NUMBER: U.S. 60/508,225
 ; PRIOR FILING DATE: 2003-10-02
 ; PRIOR APPLICATION NUMBER: U.S. 60/552,084
 ; PRIOR FILING DATE: 2004-03-11
 ; NUMBER OF SEQ ID NOS: 248
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 10
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-874-923-10

Query Match 68.6%; Score 1378; DB 5; Length 311;
 Best Local Similarity 80.0%; Pred. No. 1.6e-122;
 Matches 244; Conservative 31; Mismatches 30; Indels 0; Gaps 0;
 QY 71 LQAHAMERKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPSPFRACFKSIFR 130
 Db 7 LQAHAMERKEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGRPPMPSPFRACFKSIFR 66
 QY 131 IHTETGNIWTHLLGFLVFLFLGILTLMLRPNMYFMAPLQEKVFGMFFLGAVALCLSPSWLF 190
 Db 67 IHTETGNIWTHLLGCVFFLCIGIFYMFRPNISFVAPLQEKVFGMFFLGAVALCLSPSWLF 126
 QY 191 HTVYCHSEKVSRTSKLDYSGIALLIMSGFVPMWLYSYFYCSQPRLIYLSIVCVLGISAI 250
 Db 127 HTVYCHSEGVSRFLSKLDYSGIALLIMSGFVPMWLYSYFYCNPCFTYILIVICVLGIAAI 186
 QY 251 IVAQWDRFATPKHRTQAGVFLGLGLSGVPTMHFTIAEGFVKATTVQMGWFFLMAVY 310
 Db 187 IVSQWDMFATPQYGRAGVFLGLGLSGIIPTHLVISEGFLKAATIRQIGWMLMASLY 246
 QY 311 ITGAGLYAARIPIPERFPKFDIWFQSHQIFHVLVVAAPVHFYGVSNLQEFRYGLEGGCT 370
 Db 247 ITGAALYAARIPIPERFPKCDIWFHSHQIFHIFVVGAGFVHFHGVSNLQEFRFMIGGCT 306
 QY 371 DITLL 375
 Db 307 EEDAL 311

Search completed: April 19, 2006, 14:23:44
 Job time : 128.967 secs

Db 302 LKHLIT-FWQPEALHTGYEILMLGLYLGLGAVVYATRIPEWRMPGKFDIAGHSHQLFHV 360
QY 343 LVVAAAFVHF 352
Db 361 LVVAGALTHY 370

RESULT 5
S61982
probable membrane protein YOL002c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O2501; hypothetical protein UND327
C:Species: Saccharomyces cerevisiae
C>Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 31-Dec-2004
C:Accession: S61982; S66683; S72131
R:Starky, F.; Uhlen, M.
submitted to the EMBL Data Library, December 1995
A:Reference number: S61981
A:Accession: S61982
A:Molecule type: DNA
A:Residues: 1-327 <STE>
A:Cross-references: UNIPROT:Q12442; UNIPARC:UPI000006AC11; EMBL:U43491; NID:g1150992; P1
R:Pettersson, B.; Starky, F.; Uhlen, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66682
A:Accession: S66683
A:Molecule type: DNA
A:Residues: 1-327 <PET>
A:Cross-references: UNIPARC:UPI000006AC11; EMBL:Z74744; NID:g1419762; PIDN:CNA99001.1; F
A:Experimental source: strain S288C
R:Starky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.
Yeast 12, 1091-1095, 1996
A:Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sacchar
A:Reference number: S72130; MUID:97051599; PMID:8896276
A:Accession: S72131
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-327 <STM>
A:Cross-references: UNIPARC:UPI000006AC11; EMBL:U43491; NID:g1150992; PIDN:AAC49478.1; F
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C:Genetics:
A:Cross-references: SGD:S0005362
A:Note: YOL002c
A:Map position: 15L
C:Superfamily: Adiponectin receptor protein and homologs
C:Keywords: transmembrane protein
F;93-109/Domain: transmembrane #status predicted <TM1>
F;126-142/Domain: transmembrane #status predicted <TM2>
F;164-180/Domain: transmembrane #status predicted <TM3>
F;191-207/Domain: transmembrane #status predicted <TM4>
F;225-241/Domain: transmembrane #status predicted <TM5>
F;255-271/Domain: transmembrane #status predicted <TM6>
F;294-310/Domain: transmembrane #status predicted <TM7>

Query Match 23.6%; Score 474; DB 2; Length 327;
Best Local Similarity 38.4%; Pred. No. 5.6e-31;
Matches 104; Conservative 45; Mismatches 116; Indels 6; Gaps 2;

QY 93 RVIPYDVLPMKNDYLLHGHRRPMPSPRACFKSIPRIHTETGNIWTHL---LGVFLFL 149
Db 48 RLYSDWDEIPWQRDNDPILHGYVYKETSSTFETPKSLFYLNHESVNIYSHLIPALGFPTVL 107
QY 150 FLGILTMLRNNMYFMAPLQEKVVGFFGAVLCLSFSLFHTVYCHSEKVSRTESKLDY 209
Db 108 LDKSTI---KVATTWLDHMDWIDLFYSGAFACLILSSFHCLKSHSLRIATLGNKLDY 164
QY 210 SGIALIMGSFVFWLYYFSCSPQPLIYLSIVCVLGISAIIVQWDRFATPKRQTRAG 269
Db 165 LGICILIVTSWVILYGYEKEKSLFCLFALITVSGIACSIYSLKDKFKRWRPVRAG 224
QY 270 VFLGLGLSGVVPTMHTFIAGSGFKVATTVGQMGFFLMVMVYITGAGLYAARIIPERFPKG 329
Db 225 LFVCFGLSSIPIFSGLYCYFSFSRIWTQILFWLLGGVLYITGAVLYGNRFPPEKICPGK 284

QY 330 FDIWFQSHQIFHVLVVAFAAFVHFVGVSNLQE 360
Db 285 FDIWGHSHQLFHLVVLVIAALCHLRGLNSYE 315

RESULT 6

B85361
hypothetical protein AT4g30850 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C:Accession: B85361
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: B85361
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: UNIPROT:O65564; UNIPARC:UPI00000A9BDD; GB:NC_001268; NID:g7269986; F
C:Genetics:
A:Gene: AT4g30850
A:Map position: 4
C:Superfamily: Adiponectin receptor protein and homologs
Query Match 21.8%; Score 437; DB 2; Length 405;
Best Local Similarity 35.1%; Pred. No. 7.2e-28;
Matches 106; Conservative 42; Mismatches 118; Indels 36; Gaps 5;
QY 93 RVIPYDVLPMKNDYLLHGHRRPMPSPRACFKSIPRIHTETGNIWTHLGLFVLP---- 148
Db 30 RLMKFEELPRYLKDNF-IHNHYRCWSIKETFLSAFSGMHNELNIWTHLCLCGFAIPTWMM 88
QY 149 -----LFLGLTLMRPNMYFMAPLQEKVVGFFGAVLCLSFHTVYCHSEKVSRTESKLDY 181
Db 89 VVSMETTELGLAGFVLLSGKIKQISIFLGLDLWLMTVEQQAGHGRQWCKQKMFSPAI 148
QY 182 -LCLSFSLFHTVYCHSEKVSRTESKLDYSGIALIMGSFVFWLYYFSCSPQPLIYLS 240
Db 149 KLCITS--MSHLFACHSRRLFFWRLDYAGISLMVCSFFAPYIYAFSCHTYWRLFYLS 206
QY 241 IVCVLGISAIIVQWDRFATPKRQTRAGVFLGLSLGVVPTMHTFIAGSGFKVATTVGQM 300
Db 207 SISILGLLAIFTLSPSLSAPRFRFRAALFLTMGFSGVIPATHVLYLHKDHPNVLIA-L 265
QY 301 GWFFFLMVMYITGAGLYAARIIPERFPKGKFDIWFQSHQIFHVLVVAFAAFVHFVGVSNLQE 360
Db 266 VTELAMVLDIATGAAPFYVTRIPERWRPGAFDIAGHSHQIFHVVVVLGALAHVASLLIND 325
QY 361 FR 362
Db 326 FR 327

RESULT 7

B84633
hypothetical protein At2g24150 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: B84633
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <STO>
A:Cross-references: UNIPROT:Q9ZUH8; UNIPARC:UPI000001788DA; GB:AE002093; NID:g4115375; P
C:Genetics:

A;Gene: At2g24150
A;Map position: 2
C;Superfamily: Adiponectin receptor protein and homologs

Query Match 21.5%; Score 431.5; DB 2; Length 301;
Best Local Similarity 35.7%; Pred. No. 1.5e-27;
Matches 101; Conservative 46; Mismatches 91; Indels 45; Gaps 5;

QY 93 RVIPDYVLDWLDKNDYLLHGRPPMPSPFRACPKSIFRIHTETGNIWT-----140
DB 21 RLMKFDLPYLKDNDF-IHHYRCQMSLKOTFLSAFSWNETLNITWTFEIDFVEILII 79

QY 141 --HLGLGVFLFLGILTLMLRPNNYFMAPLQEKVFGMFFLGAVLCLFSFWLFTVYCHSE 198
DB 80 VRHLIGFGLPLMTVVSCLTETTESLAGV-----FNGAGYEPFPPSVSHLLACHSK 130

QY 199 KVSRTFSKLDYSGLIALLMGSPFWMLYYSFYCSPQRLIYLSIVCVLGISAIIVAQWDRF 258
DB 131 RFNVFFWRLLDYAGISLMIVASFPPIYVAFSCHPNFRLYLSISILGLLAIITLLSPAL 190

QY 259 ATPKHKRQTRAGVFLGLSGVVPMTFT-----TAEGFVKATTYQMGWFFLMAV 308
DB 191 STFRFPFRANLFLANGSAVIFATHVLCLYNDHPNVFIALGYEIAI-----AL 239

QY 309 MYITGAGLYAARIPERFFPGKDFIMFQSHQIHVLVVAFAFVH 351
DB 240 SYFVGATFYVSRPERKPGAFDMAGHSQIHFFVFMGALAH 282

RESULT 8

S69659
hypothetical protein YDR492w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 31-Dec-2004
C;Accession: S69659; S69664
R;Dietrich, F.S.
A;Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.
A;Reference number: S69554
A;Accession: S69659
A;Molecule type: DNA
A;Residues: 1-316 <DIE>
A;Cross-references: UNIPROT:Q03419; UNIPARC:UPI000006B9A1; EMBL:U33050; NID:g927726; PID

submitted to the EMBL Data Library, August 1995
A;Reference number: S69554
A;Accession: S69659
A;Molecule type: DNA
A;Residues: 1-316 <DIE>
A;Cross-references: UNIPROT:Q03419; UNIPARC:UPI000006B9A1; EMBL:U33050; NID:g927726; PID
C;Genetics:
A;Gene: MIPS:YDR492w
A;Map position: 4R
C;Superfamily: Adiponectin receptor protein and homologs

Query Match 20.3%; Score 407; DB 2; Length 316;
Best Local Similarity 35.8%; Pred. No. 1.5e-25;
Matches 97; Conservative 43; Mismatches 109; Indels 22; Gaps 5;

QY 97 YDVLDPWLKNDYLLHGRPPMPSPFRACPKSIFRIHTETGNIWTHLL-GFVLFLLGILT 155
DB 43 FDELPEWQKNDKILGYVRETLNWKCLYSLFYWNNETVNIYTHLVPALVYFVFAITLT 102

QY 156 MLRPNMYFMAPL-----QEKVVFGMFFLGAVLCLFSFWLFTVYCHSEKVSRTFSKLDY 209
DB 103 -----NYFLIPVPFSTSDYTTVINIFLMGAFSCLCMSCSFCHMKQHSKQSNFWSKLDY 157

QY 210 SGFALLMGSPFWMLYYSFYCSPQRLIYLSIVCVLGISAIIVAQWDRFATPKHKRQTRAG 269
DB 158 LGHISLISCMIDIIYFGFDHISYSLFTIVTLVLATCTVCVLHDKENTSTFRPPFRAM 217

QY 270 VFLGLGLSGVVPMTHTTIAEGFVKATTVG-----QMGWFFLMAVMYITGAGLYAARIPER 324
DB 218 FFTLFGFSGLLP-----LTTGPFKGIQGVNLRIKVSFVFEALFYISGAVIYGRIPET 272

QY 325 FPGKEDIMFQSHQIHVLVVAFAFVHFGV 355
DB 273 LAPGKDFPFGSSHQIHFHIMVVLGVSCHLKAI 303

RESULT 9

S62569
probable transmembrane protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C;Accession: T38588; S62569
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21801
A;Accession: T38588
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-442 <PE2>
A;Cross-references: UNIPROT:Q09910; UNIPARC:UPI000013A0ED; EMBL:Z67961; NID:g1065887; P1

A;Experimental source: strain 972h-; cosmid c30D11
C;Genetics:
A;Gene: SPAC30D11.11
A;Map position: 1L
C;Superfamily: Adiponectin receptor protein and homologs

Query Match 18.5%; Score 372; DB 2; Length 442;
Best Local Similarity 31.3%; Pred. No. 1.5e-22;
Matches 101; Conservative 48; Mismatches 136; Indels 38; Gaps 9;

QY 68 TLPLQA-----HHAMEKMEEFVYK-----VME-----GRMRVIPDYVLP 101
DB 116 TFPKAKQKALTFLHHLRLDLDYAEKSKNNVETLMTDIDKDVVEHAAKLGAKRLITLEELP 175

QY 102 DWLKDNDYLLHGRPPMPSPFRACPKSIFRIHTETGNIWTHLLGFLVFLFLGILTLMLRP-- 159
DB 176 VQHNPNYIIIRGYR-FYTSKRKCFRSLSNHNETFNITWTHLSAFT--VFPALVAYFYFSS 232

QY 160 NMYFMAPLQEKVFGMFFLGAVLCLFSFWLFTVYCHSE-KVSRFTSKLDYSGLIALLMG 218
DB 233 SSWSSVSNRIVRIFRLLSAMKCLGCSVWHITFSSLSNRYKMKRCAACMDYVIGISALLTA 292

QY 219 SFVPWLYYSFYCSPQRLIYLSIVCVLGISAIIVAQWDRFATPKHKRQTRAGVFLGLGSG 278
DB 293 SIISVEYHAFVCCQPLRFIFTGLTGLIGIYTPKKWNEKYKRSVKIFFFVGLACSG 352

QY 279 VVPTMHFTIAGFVKAT--TVQMGWFFLMAVMYITGAGLYAARIPERFFPGKEDIMFQ 336
DB 353 LIP-----MITMFYIKGTRTKYLDVPKSFISFYIIGLVFYGLHPIERFLPFGKFDIIGNS 408

QY 337 HQIHFVLVVAFAFVHFGVSNLQ 359
DB 409 HQIMHIAIIVGAFHYTGVRFE 431

RESULT 10

S64850
probable membrane protein YLR023c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein Li726
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: S64850
R;Obermaier, B.; Piravandi, E.; Rinke, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64845
A;Accession: S64850
A;Molecule type: DNA
A;Residues: 1-543 <OBE>
A;Cross-references: UNIPROT:Q07959; UNIPARC:UPI000006A56D; EMBL:Z73195; NID:g1360329; P1

A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YLR023c
A;Cross-references: SGD:S0004013
A;Map position: 12R
C;Keywords: transmembrane protein
F;261-277/Domain: transmembrane #status predicted <TM1>
F;297-313/Domain: transmembrane #status predicted <TM2>
F;338-354/Domain: transmembrane #status predicted <TM3>
F;398-414/Domain: transmembrane #status predicted <TM4>

F:431-447/Domain: transmembrane #status predicted <TMS>

Query Match 12.5%; Score 251; DB 2; Length 543;
 Best Local Similarity 24.0%; Pred. No. 1.3e-12;
 Matches 80; Conservative 48; Mismatches 132; Indels 74; Gaps 9;
 QY 90 GRWRVYPYDVLPMKNDYLLHGRPPMPSPACPKSIFRI-----HTETGNIWTHLL 143
 DB 211 GETQHLHYQLPFPFRENRYIIHGYR----FYNTSHSKSLISIFNMYGWNETSNIWSHLL 266
 QY 144 GFVLFPLFLGLTLMLRPNMY--FWAPLQEKVVFQWPFGLGAVLCLSFGLFHTVYCHS-EKV 200
 DB 267 GAIYIYLAIDYFPQSEWNSQVPPQARWVFVFLAAAKCMSSVFWHTFNGTSFLKL 326
 QY 201 SRTFSKLDYSGIALLMGSPVWLYSYFCSPQRIYLSIVCLGISAIIVQAQDRFAT 260
 DB 327 RSKFACVDYSGITILITASLTTEFTVMYSCYWMYMSISLALGVFGVFNWNSRPRDR 386
 QY 261 PKHROTQAGVFLGLGSGVVPVTHFTIAGFVKATTVGQWGP-----FLMAVMYITGAGL 316
 DB 387 PEARPLRIRPFILLATMGVLSFLHLIFLTLHVAATL-----PSPVTYKSVVYLVGVVF 441
 QY 317 YAARIPERF-----FPGKEDI----- 332
 DB 442 YGSFIPERPRSDVQDKTIPTNYELSTDLIITKQREIHFPREVPTAHSKCSCFSAKSF 501
 QY 333 ----WFQ-----SHQIFHLVVAFAAFVHFVGSNL 358
 DB 502 KSLWWDYFCCSTHFWFFVLGVIGHYRAIDM 535

RESULT 11

H84832
 hypothetical protein At2g40710 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
 C:Accession: H84832
 R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 eus, D.; Niernman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: H84832
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-93 <STO>
 A:Cross-references: UNIPROT:Q7XJN5; UNIPARC:UPI00001623F9; GB:AE002093; NID:g4895222; PI
 C:Genetics:
 A:Gene: At2g40710
 A:Map position: 2
 C:Superfamily: Adiponectin receptor protein and homologs

Query Match 8.6%; Score 173.5; DB 2; Length 93;
 Best Local Similarity 47.6%; Pred. No. 3.5e-07;
 Matches 39; Conservative 12; Mismatches 24; Indels 7; Gaps 2;
 QY 274 LGLSGVVPTWHFTIA-----EGFVKATTVGQWGFPLMAVMYITGAGLYAARIPERFPKGF 330
 DB 1 MGFSGLAPILHKLIIIFWDQPEALHTTCYBI-----LMGLLYGLGALVYATRIPIRPMWPKF 56

QY 331 DINFQSHQIFHLVVAFAAFVHF 352

DB 57 DIAGHSHQLFHLVVAAGAFTHY 78

RESULT 12

T05657
 hypothetical protein F22113.60 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
 C:Accession: T05657
 R.; Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.H.

submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15420
 A:Accession: T05657
 A:Molecule type: DNA
 A:Residues: 1-108 <BEV>
 A:Cross-references: UNIPROT:Q9SVF6; UNIPARC:UPI00000A86C0; EMBL:AL035539
 A:Experimental source: cultivar Columbia; BAC clone F22113
 C:Genetics:
 A:Map position: 4
 A:Introns: 3/3; 42/1
 A:Note: F22113.60
 C:Superfamily: Adiponectin receptor protein and homologs

Query Match 8.4%; Score 168; DB 2; Length 108;
 Best Local Similarity 45.3%; Pred. No. 1.1e-06;
 Matches 39; Conservative 10; Mismatches 31; Indels 6; Gaps 1;
 QY 273 GGLSGVVPVTHFTIAGFVKATTVGQ-----MGFFFLMAVMYITGAGLYAARIPERFP 326
 DB 8 GCGERAVSNEARSIQDIIVTAVIVTRREDIYLTGTILMGLYGLGALVYATRIPIRWM 67
 QY 327 PGKFDIWFQSHQIFHLVVAFAAFVHF 352
 DB 68 PGKFDIAGHSHQLFHLVVAAGAFTHY 93

RESULT 13

E83042
 conserved hypothetical protein PA4833 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2004
 C:Accession: E83042
 R.; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: E83042
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-205 <STO>
 A:Cross-references: UNIPROT:Q9HUX7; UNIPARC:UPI00000C5E2E; GB:AE004896; GB:AE004091; NI
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4833
 C:Superfamily: hemolysin III

Query Match 7.5%; Score 151.5; DB 2; Length 205;
 Best Local Similarity 24.6%; Pred. No. 5.1e-05;
 Matches 62; Conservative 36; Mismatches 87; Indels 67; Gaps 11;
 QY 132 HTETGNIWTHLLGFLV----PLFLGILTMLRPNMYFMAPLQEKV-FGMFFLGAVALCLSF 186
 DB 3 HGERLMAWTHLLGAVAACTGAVLTVQASLNSPW-----XIVGVGYGVTLTLTLYSI 55

QY 187 SWLFHTVYCHSKVSRFTSKLDYSGIALLIMSGFVPMYYSFYSPQPRLIYLSIVCVLG 246
 DB 56 STAYHSVRCRAKVMR---KLDHLSIYLLIAGSYTP-----FC-----LVTLRG 96

QY 247 ISAIIVQAQDRPATPKHROTQAGVFLGLSGVVPVTHFTIAGFVKATTVGQWGFLLM 306
 DB 97 -----PMG-----WTLFGIWMGLAVLQMLQIKPRSEARVLSSVVVIYAVMGWIVLI 141

QY 307 AVMYI-----TGAGLYAARIPERFPKGFDFWFSQHQIFHLVVAFAAFVHFV 353
 DB 142 AVKPLLAALGSAGFTWLAAGGVLYTVGVYAYDHRFRW---HGIWHLFVIAGSLILHFV 198

QY 354 GVSNLQEPFRL 365

DB 199 AI-----WRYVL 205

<p>RESULT 14</p> <p>S59967</p> <p>hemolysin III - Bacillus cereus</p> <p>N;Alternate names: hemolytic factor</p> <p>C;Species: Bacillus cereus</p> <p>C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 31-Dec-2004</p> <p>C;Accession: S59967; S52296</p> <p>R;Baiba, G.E.; Kuzmin, N.P.</p> <p>Biochim. Biophys. Acta 1264, 151-154, 1995</p> <p>A;Title: Cloning and primary structure of a new hemolysin gene from Bacillus cereus.</p> <p>A;Reference number: S59967; MUID:96085115; PMID:7495855</p> <p>A;Accession: S59967</p> <p>A;Status: preliminary</p> <p>A;Molecule type: DNA</p> <p>A;Residues: 1-219 <BAI></p> <p>A;Cross-references: UNIPROT:P54176; UNIPARC:UPI000012C94B; EMBL:X84058; NID:G662879; PID</p> <p>C;Superfamily: hemolysin III</p>		<p>Query Match 7.4%; Score 149; DB 2; Length 219;</p> <p>Best Local Similarity 24.3%; Pred. No. 8.8e-05;</p> <p>Matches 59; Conservative 47; Mismatches 75; Indels 62; Gaps 13;</p>	
QY	131	IHTETGNITWHLGFLVFLGLTLMRLPNMYPMAFLQKVVFGMFLGAVLCLSFWL	190
DB	12	KEEIANATHGIGAILSPALIILIIHASKHGTA--SAVVAFTVYGVSMFLLYLFS	69
QY	191	HTVYCHSEKVSRTFSKLDYSGIALLINGSFVPMLYSYFCSQPRLIYLSIVCVL	250
DB	70	HSI--HHPKVEKLTILDHSAIYLLIAGTYTPEL-----LITLRGPLG----	110
QY	251	IVAQWDRFATPKHQTRAGVFLGLSGVVPTMHTIAEGFVKATTVGQ--MGWFLMAV	308
DB	111	-----W-----TLALIIWTLAGGIIFKIFF--VRRFIKASTLCYIIIMGLII	154
QY	309	--MY--ITGAG-----LYAARIPERFFPGKFDINQ---SHQIFHVLVVA	352
DB	155	KPLYENLTGHGFLSLLAGGLYS--VGAIFF-----LWEKLPENHAIWHLFVL	207
QY	353	YGV 355	
DB	208	FCV 210	
<p>RESULT 15</p> <p>E97469</p> <p>hypothetical 23.8K protein in fldb-bglA intergenic region [imported] - Agrobacterium tum</p> <p>C;Species: Agrobacterium tumefaciens</p> <p>C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 31-Dec-2004</p> <p>C;Accession: E97469</p> <p>R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman,</p> <p>A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;</p> <p>Science 294, 2323-2328, 2001</p> <p>A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum</p> <p>A;Reference number: A97359; MUID:21608551; PMID:11743194</p> <p>A;Accession: E97469</p> <p>A;Status: preliminary</p> <p>A;Molecule type: DNA</p> <p>A;Residues: 1-232 <KUR></p> <p>A;Cross-references: UNIPROT:Q8UGX9; UNIPARC:UPI00000D198A; GB:AE007869; PIDN:AAK86710.1;</p> <p>C;Genetics:</p> <p>A;Gene: AGR C 1653</p> <p>A;Map position: circular chromosome</p> <p>C;Superfamily: hemolysin III</p>		<p>Query Match 7.4%; Score 149; DB 2; Length 232;</p> <p>Best Local Similarity 25.0%; Pred. No. 9.4e-05;</p> <p>Matches 56; Conservative 47; Mismatches 77; Indels 44; Gaps 13;</p>	
QY	141	HLGLFVFLFGLTLMRLPNMYPMA--PLQEKVVFGMFLGAVLCLSFWLFTHTYCHSE	198
DB	33	HGVG-IVFALIGATATLI---FYAMAWGSLSATAAWIYGLGLVACLSVSFTYN-IWPHS-	86
QY	199	KVSRFTSKLDYSGIALLINGSFVPMLYSYFY---CSPQRLIYLSIVCVLGISAIIVAQW	255

Db	87	RVKWFLRLDHSALFILLIAATYTPFLMRGIHDPLIAVMLGLIWLAAICGILLKCLFPPGRY	146
QY	256	DRFATPKHQTRAGVFLGLSGVVPTMHTIAEGFVKATTVGQMGWFLMAVVMYITGAG	315
Db	147	DRVA-----IGLYLAWGWSGI---MVVPLSSHLPVTL-----W-----LIVAGGV	185
QY	316	LYAARIPERFFPGKFDIW---FQSHQIFHVLVVAAPVHFYGV	355
Db	186	IYSLGV-----IFHWWEKLRFO-NAIWHGFFVVSAAAVHYFAV	221

Search completed: April 19, 2006, 14:03:23

Job time : 30.9318 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2006, 13:50:46 ; Search time 170.252 Seconds
(without alignments)
1554.007 Million cell updates/sec

Title: US-10-799-943-2

Perfect score: 2009

Sequence: 1 MSHKGVVVAQNGAPASNR.....SNLQEFYRLEGCTDDTL 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2009	100.0	375	1 ADRI_HUMAN	Q96A54 homo sapien
2	2009	100.0	375	2 Q53Y76_HUMAN	Q53Y76 homo sapien
3	2006	99.9	375	2 Q53H57_HUMAN	Q53H57 homo sapien
4	1967	97.9	375	2 Q6P746_RAT	Q6P746 rattus norv
5	1957	97.4	375	2 Q5V915_PIG	Q5V915 sus scrofa
6	1954	97.3	375	1 ADRI_MOUSE	Q91VH1 mus musculus
7	1954	97.3	375	2 Q53Y74_MOUSE	Q53Y74 mus musculus
8	1842	91.7	348	2 Q6S015_PIG	Q6S015 sus scrofa
9	1817	90.4	375	2 Q4PKP2_CHICK	Q4PKP2 gallus gall
10	1745	86.9	384	2 Q501Q0_XENLA	Q501Q0 xenopus lae
11	1742	86.7	379	2 Q66KJ1_XENTR	Q66KJ1 xenopus tro
12	1727	86.0	381	2 Q7ZY04_XENLA	Q7ZY04 xenopus lae
13	1604.5	79.9	377	2 Q803Q0_BRARE	Q803Q0 brachydanio
14	1573	78.3	318	2 Q4S853_TETNG	Q4S853 tetraodon n
15	1403.5	69.9	385	2 Q66K55_XENLA	Q66K55 xenopus lae
16	1403.5	69.9	386	1 ADRI_MOUSE	Q86V24 homo sapien
17	1403.5	69.9	386	2 Q53Y75_HUMAN	Q53Y75 homo sapien
18	1398.5	69.6	386	2 Q5TYU5_BRARE	Q5TYU5 brachydanio
19	1397.5	69.6	386	2 Q5UVJ1_PIG	Q5UVJ1 sus scrofa
20	1395.5	69.5	387	2 Q68ET2_XENLA	Q68ET2 xenopus lae
21	1391.5	69.3	386	1 ADRI_MOUSE	Q86K95 mus musculus
22	1391.5	69.3	386	2 Q53Y73_MOUSE	Q53Y73 mus musculus
23	1387.5	69.1	364	2 Q4RH94_TETNG	Q4RH94 tetraodon n
24	1384.5	68.9	386	2 Q5ZMH3_CHICK	Q5ZMH3 gallus gall
25	1372.5	68.3	386	2 Q4PKP1_CHICK	Q4PKP1 gallus gall
26	1083	53.9	206	2 Q5MIA8_PIG	Q5MIA8 sus scrofa
27	1016.5	50.6	444	1 ADRL_DROME	Q5VCV8 drosophila
28	971.5	48.4	324	2 Q7PQ98_ANOGA	Q7PQ98 anopheles g
29	940	46.8	217	2 Q6SQ14_PIG	Q6SQ14 sus scrofa
30	908	45.2	434	1 ADRL_CABEL	Q94177 caenorhabdi
31	898	44.7	433	2 Q61U91_CAEBR	Q61U91 caenorhabdi

32	876	43.6	586	2	Q61UT2_CAEBR	Q61ut2 caenorhabdi
33	873.5	43.5	581	2	Q9N536_CABEL	Q9n536 caenorhabdi
34	761	37.9	395	2	Q5DGS4_SCHJA	Q5dgs4 schistosoma
35	632	31.5	117	2	Q512P6_PIG	Q512p6 sus scrofa
36	603	30.0	114	2	Q6T5C5_BOVIN	Q6t5c5 bos taurus
37	595	29.6	318	2	Q5B3E8_EMENI	Q5b3e8 aspergillus
38	589	28.3	321	2	Q521M8_MAGGR	Q521m8 magnaporthe
39	573	28.5	321	2	Q4WXS9_ASPFU	Q4wxs9 aspergillus
40	560	27.9	139	2	Q6T5C4_BOVIN	Q6t5c4 bos taurus
41	530.5	26.4	324	1	ADRL_SCHFO	Q09749 schizosacch
42	515	25.6	315	2	Q7S0E1_NEUCR	Q7s0e1 neurospora
43	506.5	25.2	385	2	Q9SZG0_ARATH	Q9szg0 arabidopsis
44	491.5	24.5	374	2	Q67ZB8_ARATH	Q67zb8 arabidopsis
45	491	24.4	624	2	Q4PDS6_USTMA	Q4pds6 ustilago ma

ALIGNMENTS

RESULT 1
ADRI_HUMAN STANDARD; PRT; 375 AA.
AC Q96A54: Q9Y360;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Adiponectin receptor protein 1 (Progestin and adipoo receptor family member I).
GN Name=ADIPOR1; Synonyms=PAQR1; ORFNames=CGI-45;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=10810993; DOI=10.1101/gr.10.5.703;
RA Lai C.-H., Chou C.-Y., Chang L.-Y., Liu C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
RL Genome Res. 10:703-713(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Lung, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klaunig R.D., Collins P.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalek U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
TISSUE=SUBUNIT, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX MEDLINE=22687101; PubMed=12802337; DOI=10.1038/nature01705;
RA Yamauchi T., Kamon J., Ito Y., Tsuchida A., Yokomizo T., Kita S.,
Sugiyama T., Miyagishi M., Hara K., Tanoda M., Murakami K.,
Ohteki T., Uchida S., Takekawa S., Waki H., Tsuno N.H., Shibata Y.,
Terauchi Y., Froguel P., Tobe K., Koyasu S., Taira K., Kitamura T.,
Shimizu T., Nagai R., Kadowaki T.;

"Cloning of adiponectin receptors that mediate antidiabetic metabolic effects";
 Nature 423:762-769(2003).
 CC -1- FUNCTION: Receptor for globular and full-length adiponectin (APM1), an essential hormone secreted by adipocytes that acts as an antidiabetic. Probably involved in metabolic pathways that regulate lipid metabolism such as fatty acid oxidation. Mediates increased AMPK, PPARA ligand activity, fatty acid oxidation and glucose uptake by adiponectin. Has some high-affinity receptor for globular adiponectin but low-affinity receptor for full-length adiponectin.
 CC -1- SUBUNIT: May form homo and heteromultimers.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Localized to the cell membrane and intracellular organelles.
 CC -1- TISSUE SPECIFICITY: Widely expressed. Highly expressed in skeletal muscle. Expressed at intermediate level in brain, heart, spleen, kidney, liver, placenta, lung and peripheral blood leukocytes.
 CC Weakly expressed in colon, thymus and small intestine.
 CC -1- SIMILARITY: Belongs to the ADIPOR family.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 369.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC ENBL; AF151803; AAD34040.1; ALT FRAMES; mRNA.
 CC DR ENBL; BC001594; AAH01594.1; -; mRNA.
 CC DR ENBL; BC010743; AAH10743.1; -; mRNA.
 CC DR Ensembl; ENSG00000159346; Homo sapiens.
 CC DR HGNC; HGNC:24040; ADIPOR1.
 CC MIM; 607945; -
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0042562; P:hormone binding; IDA.
 CC GO; GO:0019395; P:fatty acid oxidation; IDA.
 CC GO; GO:0009755; P:hormone-mediated signaling; IDA.
 CC DR InterPro; IPR004254; HlyIII_related.
 CC DR Pfam; PF03006; HlyIII; 1.
 CC Fatty acid metabolism; Lipid metabolism; Receptor; Transmembrane.
 CC TOPO_DOM 1 136 Cytoplasmic (Potential).
 CC TRANSMEM 137 157 1 (Potential).
 CC TOPO_DOM 158 170 Extracellular (Potential).
 CC TRANSMEM 171 191 2 (Potential).
 CC TOPO_DOM 192 209 Cytoplasmic (Potential).
 CC TRANSMEM 210 230 3 (Potential).
 CC TOPO_DOM 231 235 Extracellular (Potential).
 CC TRANSMEM 236 256 4 (Potential).
 CC TOPO_DOM 257 267 Cytoplasmic (Potential).
 CC TRANSMEM 268 288 5 (Potential).
 CC TOPO_DOM 289 296 Extracellular (Potential).
 CC TRANSMEM 297 317 6 (Potential).
 CC TOPO_DOM 318 331 Cytoplasmic (Potential).
 CC TRANSMEM 332 352 7 (Potential).
 CC TOPO_DOM 353 375 Extracellular (Potential).
 CC SEQUENCE 375 AA; 42616 MW; 1CC0300A7D178EB0 CRC64;
 Query Match 100.0%; Score 2009; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2e-154;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVVAQNGAPASNRADTVLAELGLPLEEKGKRVIANPPKAEETCTCPVQEE 60
 DB 1 MSHKGSVVAQNGAPASNRADTVLAELGLPLEEKGKRVIANPPKAEETCTCPVQEE 60
 QY 61 EEEVRVLTLPLOAHAMEKEEFVYKWEGRWRVIPYDVLPDWLKNDYLLHGRPPMPS 120
 DB 61 EEEVRVLTLPLOAHAMEKEEFVYKWEGRWRVIPYDVLPDWLKNDYLLHGRPPMPS 120
 QY 121 FRACPKSIFRIHTETGNITWHLGLFVLFLGILTLMLRPNNYFMAPLOEKVVFQGFLLGA 180
 DB 121 FRACPKSIFRIHTETGNITWHLGLFVLFLGILTLMLRPNNYFMAPLOEKVVFQGFLLGA 180

RT 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQRLIYLS 240
 RL 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQRLIYLS 240
 CC 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVQGM 300
 CC 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVQGM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE 360
 DB 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE 360
 QY 361 FRYLEGSGCTDDTL 375
 DB 361 FRYLEGSGCTDDTL 375
 RESULT 2
 Q33YV6 HUMAN PRELIMINARY; PRT; 375 AA.
 ID Q33YV6_HUMAN PRELIMINARY; PRT; 375 AA.
 AC Q33YV6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Progestin and adipoQ receptor family member I.
 GN Name=PAQR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RA Tang Y.T., Hu T., Arterburn M., Boyle B., Bright J., Emtage P.,
 RA Funk W.;
 RT "PAQR proteins: a novel membrane receptor family defined by an ancient 7-transmembrane pass motif."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBAJ databases.
 DR EMBL; AY424279; AAR08367.1; -; mRNA.
 KW Receptor.
 SQ SEQUENCE 375 AA; 42615 MW; 1CC0300A7D178EB0 CRC64;
 Query Match 100.0%; Score 2009; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2e-154;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSHKGSVVAQNGAPASNRADTVLAELGLPLEEKGKRVIANPPKAEETCTCPVQEE 60
 DB 1 MSHKGSVVAQNGAPASNRADTVLAELGLPLEEKGKRVIANPPKAEETCTCPVQEE 60
 QY 61 EEEVRVLTLPLOAHAMEKEEFVYKWEGRWRVIPYDVLPDWLKNDYLLHGRPPMPS 120
 DB 61 EEEVRVLTLPLOAHAMEKEEFVYKWEGRWRVIPYDVLPDWLKNDYLLHGRPPMPS 120
 QY 121 FRACPKSIFRIHTETGNITWHLGLFVLFLGILTLMLRPNNYFMAPLOEKVVFQGFLLGA 180
 DB 121 FRACPKSIFRIHTETGNITWHLGLFVLFLGILTLMLRPNNYFMAPLOEKVVFQGFLLGA 180
 QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQRLIYLS 240
 DB 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPLWLYSYFCSPQRLIYLS 240
 QY 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVQGM 300
 DB 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGSLGVVPTMHFTIAEGFVKATVQGM 300
 QY 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE 360
 DB 301 GWFFLMAVMYITGAGLYAARIPERFFPKGFDIWFQSHQIFHVLVVAAPVHFYGVSNLQE 360
 QY 361 FRYLEGSGCTDDTL 375
 DB 361 FRYLEGSGCTDDTL 375

```

Db      361  FRYGLEGGCTDDTLL 375
RESULT 3
Q53HS7 HUMAN
ID      Q53HS7_HUMAN PRELIMINARY; PRT; 375 AA.
AC      Q53HS7;
DT      13-SEP-2005 (TrEMBLrel. 31, Created)
DT      13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT      13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE      Adiponectin receptor 1 variant (Fragment).
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Adipose tissue;
RA      Maruyama K., Sugano S.;
RT      "Oligo-capping: a simple method to replace the cap structure of
RT      eucaryotic mRNAs with oligoribonucleotides.";
RL      Gene 138:171-174(1994).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Adipose tissue;
RA      Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT      "Construction and characterization of a full length-enriched and a 5'-
RT      end-enriched cDNA library.";
RL      Gene 200:149-156(1997).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Adipose tissue;
RA      Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA      Tanaka A., Yokoyama S.;
RL      Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AK225203; BAD96223.1; -; mRNA.
KW      Receptor.
FT      NON TER.
SQ      SEQUENCE 375 AA; 42631 MW; 1CC03019C52C1EB0 CRC64;

Query Match 99.9%; Score 2006; DB 2; Length 375;
Best Local Similarity 99.7%; Pred. No. 3.5e-154;
Matches 374; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  MSHKGSVVAQNGAPASNREADTVLAEIPLLEKGRKRVIANPPKABEEQTCVPVQEE 60
DB      1  MSHKGSVVAQNGAPASNREADTVLAEIPLLEKGRKRVIANPPKABEEQTCVPVQEE 60

QY      61  EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGHRRPMP 120
DB      61  EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGHRRPMP 120

QY      121  FRACFKSIPIRHTETGNITWLLGFLVFLGLITLMLRPNMYPMAIPLQEKVFGMFLGA 180
DB      121  FRACFKSIPIRHTETGNITWLLGFLVFLGLITLMLRPNMYPMAIPLQEKVFGMFLGA 180

QY      181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLINGSFVPLYYSFYCSPOPRLIYLS 240
DB      181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLINGSFVPLYYSFYCSPOPRLIYLS 240

QY      181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLINGSFVPLYYSFYCSPOPRLIYLS 240
DB      181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLINGSFVPLYYSFYCSPOPRLIYLS 240

QY      241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGFVKATTVGQM 300
DB      241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGFVKATTVGQM 300

QY      301  GWFFLMAVMTITAGLYAARIPERFFPGKFDIWFQSHQIYHVLVAAAFVHFYGVSNLQ 360
DB      301  GWFFLMAVMTITAGLYAARIPERFFPGKFDIWFQSHQIYHVLVAAAFVHFYGVSNLQ 360

QY      361  FRYGLEGGCTDDTLL 375
DB      361  FRYGLEGGCTDDTLL 375

```

```

RESULT 4
Q6P746 RAT
ID      Q6P746 RAT PRELIMINARY; PRT; 375 AA.
AC      Q6P746;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Adiponectin receptor 1.
DE      Name=LOC289036;
GN      Rattus norvegicus (Rat).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Prostate;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA      Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Prostate;
RA      Strausberg R.;
RL      Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC061838; AAH61838.1; -; mRNA.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      InterPro; IPR004254; HlyIII_related.
DR      Pfam; PF03006; HlyIII; 1.
KW      Receptor.
SQ      SEQUENCE 375 AA; 42466 MW; 69DF07025BDCBF02 CRC64;

Query Match 97.9%; Score 1967; DB 2; Length 375;
Best Local Similarity 97.6%; Pred. No. 5.1e-151;
Matches 366; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1  MSHKGSVVAQNGAPASNREADTVLAEIPLLEKGRKRVIANPPKABEEQTCVPVQEE 60
DB      1  MSHKGSVVAQNGAPASNREADTVLAEIPLLEKGRKRVIANPPKABEEQTCVPVQEE 60

QY      61  EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGHRRPMP 120
DB      61  EBEVRVLTLPLOAHAMEKMEEFVYKWEGRWRVPIYDVLDPWLKNDYLLHGHRRPMP 120

QY      121  FRACFKSIPIRHTETGNITWLLGFLVFLGLITLMLRPNMYPMAIPLQEKVFGMFLGA 180
DB      121  FRACFKSIPIRHTETGNITWLLGFLVFLGLITLMLRPNMYPMAIPLQEKVFGMFLGA 180

QY      181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLINGSFVPLYYSFYCSPOPRLIYLS 240
DB      181  VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLINGSFVPLYYSFYCSPOPRLIYLS 240

QY      241  IVCVLGISAIIVAQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIAGFVKATTVGQM 300

```

```
Db 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIABGFVKATTVGQM 300
Qy 301 GWFFLMAVMIITAGLYAARIPERFPFGKFDIWFQSHQIHFLVAVAAAFVHFYGVSNLQ 360
Db 301 GWFFLMAVMIITAGLYAARIPERFPFGKFDIWFQSHQIHFLVAVAAAFVHFYGVSNLQ 360
Qy 361 FRYGLEGGCTDDTL 375
Db 361 FRYGLEGGCTDDSL 375

RESULT 5
QSV9L5_PIG PRELIMINARY; PRT; 375 AA.
AC QSV9L5_PIG
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Adiponectin receptor 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15542462;
RA Ding S.T., Liu B.H., Ko Y.H.;
RT "Cloning and expression of porcine adiponectin and adiponectin
RT receptor 1 and 2 genes in pigs.";
RL J. Anim. Sci. 82:3162-3174(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y.C., Liu B.H., Ding S.T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY578142; AAT72305.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR004254; HlyIII-related.
DR Pfam; PF03006; HlyIII; 1.
KW Receptor.
SQ SEQUENCE 375 AA; 42431 MW; 200C3C440883D662 CRC64;

Query Match 97.4%; Score 1957; DB 2; Length 375;
Best Local Similarity 97.3%; Pred. No. 3.3e-150;
Matches 365; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSHKGSVVAQNGAPASNRADTVLAEGLPILLEKGRKRVIANPPKABEEQTCVPQEE 60
Db 1 MSHKGFVGNQNGAPASNRADTVLAEGLPILLEKGRGTNTNPPKABEEQACVPQEE 60

Qy 61 EEEVRVLTLPLOAHAMEKEEFPYKWEGRWRVPIYDVLDPWLKNDYLLHGRHPMP 120
Db 61 EEEVRVLTLPLOAHAMEKEEFPYKWEGRWRVPIYDVLDPWLKNDYLLHGRHPMP 120

Qy 121 FRACFKSIPIRHTGTGNTWHLGFLVFLFLGILTLWLRNMYMAPLQEKVYFGMFFLGA 180
Db 121 FRACFKSIPIRHTGTGNTWHLGFLVFLFLGILTLWLRNMYMAPLQEKVYFGMFFLGA 180

Qy 181 VLCLSPFWLPHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYL 240
Db 181 VLCLSPFWLPHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPLWLYSFYCSQPRLIYL 240

Qy 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIABGFVKATTVGQM 300
Db 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGLSGVVPVTHFTIABGFVKATTVGQM 300

Qy 301 GWFFLMAVMIITAGLYAARIPERFPFGKFDIWFQSHQIHFLVAVAAAFVHFYGVSNLQ 360
Db 301 GWFFLMAVMIITAGLYAARIPERFPFGKFDIWFQSHQIHFLVAVAAAFVHFYGVSNLQ 360
Qy 361 FRYGLEGGCTDDTL 375
```

```
Db 361 FRYGLEGGCTDDSL 375
Qy 361 FRYGLEGGCTDDSL 375

RESULT 6
ADRI_MOUSE STANDARD; PRT; 375 AA.
AC Q91VH1; Q9CZAO;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Adiponectin receptor protein 1.
GN Name=Adipor1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haseizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Heston S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usgun T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```


QY 121 FRACFKSIPIRIHTETGNIWTHLLGFLVLEPLGLTLTMLRPNMYMAPLQKVVFGMPFLGA 180
 DB 121 FRACFKSIPIRIHTETGNIWTHLLGFLVLEPLGLTLTMLRPNMYMAPLQKVVFGMPFLGA 180
 QY 181 VCLCSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSPQRLIYLS 240
 DB 181 VCLCSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSPQRLIYLS 240
 QY 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGLSLGSGVVPMTMHTIABGFVKATTVGQM 300
 DB 241 IVCVLGISAIIVQWDRFATPKHQTRAGVFLGLSLGSGVVPMTMHTIABGFVKATTVGQM 300
 QY 301 GWFFLMAVMTITAGLYAARIPIRPFPGKFDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 360
 DB 301 GWFFLMAVMTITAGLYAARIPIRPFPGKFDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 360
 QY 361 FRYGLEGGCTDDTL 375
 DB 361 FRYGLEGGCTDDSL 375

RESULT 8

Q6SQ15_PIG PRELIMINARY; PRT; 348 AA.
 AC O6SQ15_PIG
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE Adiponectin receptor 1 (Fragment).
 GN Name=ADIPOR1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15705753;
 RA Lord E., Ledoux S., Murphy B.D., Beaudry D., Palin M.F.;
 RT "Expression of adiponectin and its receptors in swine.";
 RL J. Anim. Sci. 83:565-578(2005).
 DR EMBL; AV452710; AAR91794.1; -; mRNA.
 DR GO; GO:0016021; C-integral to membrane; IEA.
 DR GO; GO:0004872; F-receptor activity; IEA.
 DR InterPro; IPR004254; HlyIII-related.
 DR Pfam; PF03006; HlyIII; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 348 348
 FT SEQUENCE 348 AA; 39899 MW; 0CE2DF4F7DE6F4F8 CRC64;

Query Match 91.7%; Score 1842; DB 2; Length 348;

Best Local Similarity 98.3%; Pred. No. 6.5e-141;

Matches 342; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 27 LAELGPLLEKGRVIANPKABEEQTCVPQEESEVRVLTLPLOAHAMEKMEEFVYK 86
 DB 1 LAELGPLLEKGRGTNTNPPKABEEQACVPQEESEVRVLTLPLOAHAMEKMEEFVYK 60
 QY 87 VNEGWRVPIYDVLPMWLDNDYLLHGRHPMPSPRACFKSIPIRIHTETGNIWTHLLGFV 146
 DB 61 VNEGWRVPIYDVLPMWLDNDYLLHGRHPMPSPRACFKSIPIRIHTETGNIWTHLLGFV 120
 QY 147 LFLFLGILTMLRPNMYMAPLQKVVFGMPFLGAVLCLSFSLFHTVYCHSEKVSRTFSK 206
 DB 121 LFLFLGILTMLRPNMYMAPLQKVVFGMPFLGAVLCLSFSLFHTVYCHSEKVSRTFSK 180
 QY 207 LDYSGIALLIMSGFVPMWLYYSFYCSPQRLIYLSIVCVLGISAIIVQWDRFATPKHQ 266
 DB 181 LDYSGIALLIMSGFVPMWLYYSFYCSPQRLIYLSIVCVLGISAIIVQWDRFATPKHQ 240
 QY 267 RAGVFLGLSLGSGVVPMTMHTIABGFVKATTVGQMGWFFLMAVMTITAGLYAARIPIRPF 326

DB 241 RAGVFLGLSLGSGVVPMTMHTIABGFVKATTVGQMGWFFLMAVMTITAGLYAARIPIRPF 300
 QY 327 PKGPDINWQSHQIHVLVVAFAAFVHFYGVSNLQRYLEGCTDDTL 374
 DB 301 PKGPDINWQSHQIHVLVVAFAAFVHFYGVSNLQRYLEGCTDDTL 348

RESULT 9

Q4PKP2_CHICK PRELIMINARY; PRT; 375 AA.
 AC Q4PKP2;
 DT 13-SEP-2005 (Tremblrel. 31, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DE Adiponectin receptor 1.
 GN Name=ADIPOR1;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Hyline W36; TISSUE=Adipose tissue;
 RA Ramachandran R., Ocon O., Metzger S.;
 RT "Molecular Cloning and Tissue Expression of Chicken AdipoR1 and
 RT AdipoR2 cDNA.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; DQ072275; AAY81969.1; -; mRNA.
 KW Receptor.
 SQ SEQUENCE 375 AA; 42182 MW; 6ACBA83D24771F00 CRC64;

Query Match 90.4%; Score 1817; DB 2; Length 375;

Best Local Similarity 91.2%; Pred. No. 7.5e-139;

Matches 343; Conservative 11; Mismatches 20; Indels 2; Gaps 2;

QY 1 MSSHKGSVVAGQNGAPASNREADTVLAELGPLLEKGRVIANPPKABEEQTCVPQEE 60
 DB 1 MASRKAAAAAGNGLAAGRDRHALELAELGPLLEKGEQAGTASA-EDPPCPVAREE 59
 QY 61 EEE-VRVLTLPLOAHAMEKMEEFVYKVGWRVPIYDVLPMWLDNDYLLHGRHPMP 119
 DB 60 EEEVVRVLTLPLOAHAMEKMEEFVYKVGWRVPIYDVLPMWLDNDYLLHGRHPMP 119
 QY 120 SFRACFKSIPIRIHTETGNIWTHLLGFVLEPLGLTLTMLRPNMYMAPLQKVVFGMPFLG 179
 DB 120 SFRACFKSIPIRIHTETGNIWTHLLGFVLEPLGLTLTMLRPNMYMAPLQKVVFGMPFLG 179
 QY 180 AVLCLSPSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSPQRLIYL 239
 DB 180 AVLCLSPSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYYSFYCSPQRLIYL 239
 QY 240 SIVCVLGISAIIVQWDRFATPKHQTRAGVFLGLSLGSGVVPMTMHTIABGFVKATTVGQ 299
 DB 240 SIVCVLGISAIIVQWDRFATPKHQTRAGVFLGLSLGSGVVPMTMHTIABGFVKATTVGQ 299
 QY 300 MGWFFLMAVMTITAGLYAARIPIRPFPGKFDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 359
 DB 300 MGWFFLMAVMTITAGLYAARIPIRPFPGKFDIWFQSHQIHVLVVAFAAFVHFYGVSNLQ 359
 QY 360 EPRYGLEGGCTDDTL 375
 DB 360 EPRYGLEGGCTDDSL 375

RESULT 10

Q50100_XENLA PRELIMINARY; PRT; 384 AA.
 ID Q50100_XENLA
 AC Q50100;
 DT 13-SEP-2005 (Tremblrel. 31, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)

DE	Hypothetical protein.	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;	
OC	Xenopodinae; Xenopus; Xenopus.	
OX	NCBI_TaxID=8355;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Kidney;	
RC	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;	
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,	
RA	Richardson P.;	
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus	
RT	initiative.";	
RL	Dev. Dyn. 225:384-391(2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Embryo;	
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,	
RA	Schuerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[3]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Embryo;	
RC	Klein S., Gerhard D.S.;	
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: BC095928; AAH95928.1; -; mRNA.	
DR	Hypothetical protein.	
SQ	SEQUENCE 384 AA; 43412 MW; C979CA392887BESC CRC64;	
	Query Match 86.9%; Score 1745; DB 2; Length 384;	
	Best Local Similarity 86.4%; Pred. No. 5.3e-133;	
	Matches 325; Conservative 17; Mismatches 32; Indels 2; Gaps 1;	
Qy	2 SSHKGSVVAQNGAPANREADTVLAEGLPGLLEBKGRVIANPKAEBSQTCVPQ--E 59	
Db	9 SQGESSAPSSNSNSSSSRGEADDELTELGLPGLLETRDRIGQTSSSGDGNQAGKVSQDE 68	
Qy	60 EEEERVLTLPLQAHAMEKEEFYKVGEGRWVIPYDVLPDWLKNDYLLHGRPPM 119	
Db	69 EEEERVLTLPLQAHAMEKEEFYKVGEGRWVIPYDVLPDWLKNDYLLHGRPPM 128	
Qy	120 SFRACFKSIFRIHTETGNIWTHLLGFVFLPLGLITLMRLPNMYPMAPLQEKVFGMFFLG 179	
Db	129 SFRACFKSIFRIHTETGNIWTHLLGFVFLPLGLITLMRLPNMYPMAPLQEKVFGMFFLG 188	
Qy	180 AVLCLSPFWLPHYTYCHSEKVSRTFSKLDYSGIALLMGSPVPMWLYSPFCSPQRLIYL 239	
Db	189 AVLCLSPFWLPHYTYCHSEKVSRTFSKLDYSGIALLMGSPVPMWLYSPFCSPQRLIYL 248	
Qy	240 SIYCVLIGTSALIAVQWDRFATPKHROTQTRAGVFLGLSGVVTWHFTIAEGFVKATTVGQ 299	
Db	249 SIYCVLIGTSALIAVQWDRFATPKHROTQTRAGVFLGLSGVVTWHFTIAEGFVKATTVGQ 308	
Qy	300 MGWFFLNAVMIYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVVAFAAFVHFYGVSNLQ 359	
Db	309 MGWFFLNAVMIYITGAGLYAARIPERFFPGKFDIWFQSHQIFHVLVVAFAAFVHFYGVSNLQ 368	
Qy	360 EFRYGLGGCTDDTL 375	
Db	369 EFRYALEGGCTDDSL 384	
RESULT 11		
Q66KJ1	XENTR	
ID	Q66KJ1 XENTR PRELIMINARY; PRT; 379 AA.	
AC	Q66KJ1;	
DT	25-OCT-2004 (TrEMBLrel. 28, Created)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	Name=adipor1-prov;	
GN	Adipor1-prov protein.	
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;	
OC	Xenopodinae; Xenopus; Silurana.	
OX	NCBI_TaxID=8364;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Embryo;	
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,	
RA	Schuerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Embryo;	
RC	Klein S., Gerhard D.S.;	
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: BC080374; AAH80374.1; -; mRNA.	
DR	GO: GO:0016021; C:integral to membrane; IEA.	
DR	InterPro: IPR004254; HlyIII-related.	
DR	Pfam: PFO3006; HlyIII; 1.	
SQ	SEQUENCE 379 AA; 43006 MW; 7E07CF137A989AB7 CRC64;	
	Query Match 86.7%; Score 1742; DB 2; Length 379;	
	Best Local Similarity 86.2%; Pred. No. 9.1e-133;	
	Matches 325; Conservative 21; Mismatches 25; Indels 6; Gaps 2;	
Qy	1 MSHKGSVVAQNGAPANREADTVLAEGLPGLLEBKGRVIANPKAEBSQTCVP--PQ 58	
Db	7 LSSQGESALS---SSSSRGETDDELAELGLPLEARRRIGQTSSSGDGNQASKVSPEE 62	
Qy	59 EEEERVLTLPLQAHAMEKEEFYKVGEGRWVIPYDVLPDWLKNDYLLHGRPPM 118	
Db	63 EEEERVLTLPLQAHAMEKEEFYKVGEGRWVIPYDVLPDWLKNDYLLHGRPPM 122	
Qy	119 PSFRACFKSIFRIHTETGNIWTHLLGFVFLPLGLITLMRLPNMYPMAPLQEKVFGMFFL 178	
Db	123 PSFRACFKSIFRIHTETGNIWTHLLGFVFLPLGLITLMRLPNMYPMAPLQEKVFGMFFL 182	

```

QY 179 GAVLCISFWLFTVYCHSEKVSRTSKLDYSGIALLIMSGSFVPMLYSYFCSPQRLIY 238
Db 183 GAVLCISFWLFTVYCHSEKVSRTSKLDYSGIALLIMSGSFVPMLYSYFCSPQRLIY 242
QY 239 LSIVCVLGISAIIVAQWDRFATPKHRQTRAGVFLGLSGVPTMHFTTIAEGFVKATTVG 298
Db 243 LSIVCVLGITAIIVAQWDRFATPKHRPTRAGVFLGLSGIVPTLHFTTIAEGFVKATTVG 302
QY 299 QMGWFFLMVMYITGAGLYAARIPERFFPGKEDINFQSHQIFHVLVVAARFVHFYGVSNL 358
Db 303 QMGWFFLMVMYITGAGLYAARIPERFFPGKEDINFQSHQIFHVLVVAARFHFYGVSNL 362
QY 359 QBFYGLGGCTDITLL 375
Db 363 QBFYALGGCTDITLL 379

RESULT 12
Q72V04 XENLA
ID Q72V04 XENLA PRELIMINARY; PRT; 381 AA.
AC Q72V04;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adipor1-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044035; AAH44035.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004254; HlyIII-related.
DR Pfam; PF03006; HlyIII; 1.
SQ SEQUENCE 381 AA; 43073 MW; 1D99EB4BE767447 CRC64;

```

```

Query Match 86.0%; Score 1727; DB 2; Length 381;
Best Local Similarity 86.3%; Pred. No. 1.5e-131;
Matches 321; Conservative 18; Mismatches 31; Indels 2; Gaps 1;

QY 6 GSVAAQNGAPASNRADTVLAEIGPLLEKGRKRVIANPPKAEIEQCVPVQ--EBEEE 63
Db 10 QGECALSKSSSSSRGADDLEALGLPLLKAGRDIGTSSCGDENQAGKVSQEEEEEE 69
QY 64 VRVLTLPLOAHAMEKEEFVYKWEGRWRVTPYDVLDPDLKNDYLLHGRPPMPSRA 123
Db 70 VRVLTLPLOAHAMEKEEFVYKWEGRWRVTPYDVLDPDLKNDYLLHGRPPMPSRA 129
QY 124 CFSIFRIHTETGNIWTHLLGFLVFLGILTLRPNMYFMAPLOEKVVFGFFLGAVLC 183
Db 130 CFSIFRIHTETGNIWTHLLGFLVFLGILTLRPNMYFMAPLOEKVVFGFFLGAVLC 189
QY 184 LFSWLFHTVYCHSEKVSRTSKLDYSGIALLIMSGSFVPMLYSYFCSPQRLIYLSIVC 243
Db 190 LFSWLFHTVYCHSEKVSRTSKLDYSGIALLIMSGSFVPMLYSYFCSPQRLIYLSIVC 249
QY 244 VLGISAIIVAQWDRFATPKHRQTRAGVFLGLSGVPTMHFTTIAEGFVKATTVGQMGWF 303
Db 250 VLGITAIIVAQWDRFATPKHRPTRAGVFLGLSGIVPTLHFTTIAEGFVKATTVGQMGWF 309
QY 304 PLMAVMYITGAGLYAARIPERFFPGKEDINFQSHQIFHVLVVAARFVHFYGVSNLQEPY 363
Db 310 PLMAVMYITGAGLYAARIPERFFPGKEDINFQSHQIFHVLVVAARFHFYGVSNLQEPY 369
QY 364 GLEGCTDITLL 375
Db 370 ALEGGCTDITLL 381

RESULT 13
Q803Q0 BRARE PRELIMINARY; PRT; 377 AA.
AC Q803Q0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adiponectin receptor 1.
GN Name=adipor1b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB; TISSUE=Whole body;
RG NIH MGC Project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RM ENBL; BC044388; AAH44388.1; -: mRNA.
DR Ensembl; ENSDARG0000042717; Danio rerio.
DR ZFIN; ZDB-GENE-040426-2896; adiporib.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004254; HlyIII-related.
DR Pfam; PF03006; HlyIII; 1.
KW Receptor.
SQ SEQUENCE 377 AA; 42426 MW; D85C91CD603B19EC CRC64;

Query Match 79.9%; Score 1604.5; DB 2; Length 377;
Best Local Similarity 78.1%; Pred. No. 1.3e-121;
Matches 299; Conservative 29; Mismatches 34; Indels 21; Gaps 4;

QY 4 HKGSVVAQNGAPASNPREAD-----TVELAELGPLL-----BEKGRVIANPPKAEERQ 52
DB 5 HGGDC---GNSDAERRATDEANMEDAELSELGPLTSPANSEEGRGASDPENEDE- 60

QY 53 TCPVQBEERVRVLTPLQAHAMKMEEFYKVGWGRWVRVPIYDVLDPWLKNDNDYLLH 112
DB 61 -----KEEGRLRVTLTPMQAHAMKMEEFVHKWEGHWRVPIYHLLPDLWLKNDNDYLLH 114

QY 113 GHRPPMPSPFRACFKSIPIRIHTETGNIWTHLLGFLVFLFLGILTLMLRNMYFMAPLOEKVV 172
DB 115 GHRPPMPSPFRACFKSIPIRIHTETGNIWTHLLGFLVFLFLGILTLMLRNMYFMAPLOEKVV 174

QY 173 FGMPFLGAVLCFSWLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYFCSP 232
DB 175 FGMPFLGAVLCFSWLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYFCSP 234

QY 233 QPRLIYLSIVCVLGISALIIVAQWDRFATPKHROTFRAGVFLGLSGVVPMTHTTIAEGFV 292
DB 235 QPRLIYLSIVCVLGISALIIVAQWDRFATPKHROTFRAGVFLGLSGVVPMTHTTIAEGFV 294

QY 293 KATTVGQMGWFFLMVMYITGAGLYAARIPIERFPFGKFDIFWQSHQIFHVLVVAAPVHF 352
DB 295 KATTVGQMGWFFLMVMYITGAGLYAARIPIERFPFGKFDIFWQSHQIFHVLVVAAPVHF 354

QY 353 YGVSNLQEFYRGLGGCTDITLL 375
DB 355 YGVSNLQEFYRGLGGCTDITLL 377

RESULT 14
Q4SS53_TETNG
ID Q4SS53_TETNG PRELIMINARY; PRT; 318 AA.
AC Q4SS53;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 11 SCAF14479, whole genome shotgun sequence.
GN (Fragment).
GN ORFNames=GSTENG0013607001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Doseat C., Segurens B.,
RA Dagilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cottolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.",
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
FT EMBL; CAAE01014479; CAP96529.1; -: Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 318 AA; 36444 MW; C18F0ACFBEE28470 CRC64;

Query Match 78.3%; Score 1573; DB 2; Length 318;
Best Local Similarity 89.3%; Pred. No. 3.8e-119;
Matches 284; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 58 QBEEERVRVLTPLQAHAMKMEEFYKVGWGRWVRVPIYDVLDPWLKNDNDYLLHGRPP 117
DB 1 EDDDEVAEVLTLPLQAHAMKMEEFVHKWEGHWRVIFHVLPEWLKNDNDYLLHGRPP 60

QY 118 MPSPFRACFKSIPIRIHTETGNIWTHLLGFLVFLFLGILTLMLRNMYFMAPLOEKVFGMPF 177
DB 61 MPSPFRACFKSIPIRIHTETGNIWTHLLGFLVFLFLGILTLMLRNMYFMAPLOEKVFGMPF 120

QY 178 LGAVLCLSPWLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYFCSPORLI 237
DB 121 LGAVLCLSPWLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVFWLYSPYFCSPORLI 180

QY 238 YLSIVCVLGISALIIVAQWDRFATPKHROTFRAGVFLGLSGVVPMTHTTIAEGFVKATTV 297
DB 181 YLSIVCVLGISALIIVAQWDRFATPKHROTFRAGVFLGLSGVVPMTHTTIAEGFVKATTV 240

QY 298 GQMGWFFLMVMYITGAGLYAARIPIERFPFGKFDIFWQSHQIFHVLVVAAPVHFVGVSN 357
DB 241 GQMGWFFLMVMYITGAGLYAARIPIERFPFGKFDIFWQSHQIFHVLVVAAPVHFVGVSN 300

QY 358 LQEFYRGLGGCTDITLL 375
DB 301 LQEFYRGLGGCTDITLL 318

RESULT 15
Q6KKS5_XENLA
ID Q6KKS5_XENLA PRELIMINARY; PRT; 385 AA.
AC Q6KKS5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC85478 protein.
GN Name=MGC85478;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative",
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;


```

; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2886
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2886

Query Match      8.2%; Score 164; DB 2; Length 199;
Best Local Similarity 22.8%; Pred. No. 2.5e-09;
Matches 60; Conservative 31; Mismatches 86; Indels 86; Gaps 7;

QY 93 RVIPYDVLDMKNDYLLHGRPPMPSPRACPKSIFRIHTETGNTWTHLLGFVLEFLG 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 RLLDWASSPHLQFNKFLVTGYR-PASSGGCLRSFYLHNLGNLYAH-----G 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 153 ILTMLRPNMYFMAPLOEKVVGFMFFLGAIVLCLSFSLFHTVYCHSEKVSRTSKLDYSGI 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 ALPIIHTCTACRPLWLRPTALVGTVLSGVA-----GWRALTAPSTSA RL-RAFGW--QAAA 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 213 ALLIMSGFVPMWLYSYFYCSPQPRLIYLSIVCVLGISAIIVAOQDRPATPKRQTRAGVFL 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 RLLVFGA-----RGVGL 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 273 GGLSGVPMPTHTIAGFVKATTVGQMGWFFLMVAVYITGAGLYAARIPERFPFGKFDI 332
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 GSGAPGSLPC-----YLRMDALALLGGIVNVARLPERMGPGRFDY 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 333 WFQSHQIFHVLVVAAPVHFYGV 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 162 WGNSHQIMHLLSVGSILQLHAGV 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
US-09-902-540-14719
; Sequence 14719, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14719
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14719

Query Match      7.6%; Score 152; DB 2; Length 224;
Best Local Similarity 27.9%; Pred. No. 5.9e-08;
Matches 60; Conservative 29; Mismatches 100; Indels 26; Gaps 8;

QY 140 THLLGFVLFPLGILTMWRP--NMVFMAPLOEKVFGMFLGAVLCLSFSLFHTVYCHS 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 SHAVAFVAALLGCIQLAMPVRGPQYLA DL-----VFGG---SNVLMFGVSATYHR-FTWG 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 198 EKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFYCSPQPRLIYLSIVCVLGISAIIVAOQDR 257

```

```

Db 76 MDAYRRIQRFDAALYILIAGSFTPMATLDTTGDTSLLML-----MMIAALTGAGLTL 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 258 FATPKHQTRAGVFLGCLGSLGVVPTMHTIAGGFVKATTVGQMGWFFLMVAVYITGAGLY 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 LGVHTSRGLRSALYVAG--AVATPVMLRLPB-----VIGSGRVAWLVLGGVLIYAVGAVIY 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 318 AARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHF 352
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 ARR-----WPDPIPTVFGYHEIFHLLLVVAAGVHY 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
US-09-252-991A-26973
; Sequence 26973, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26973
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26973

Query Match      7.5%; Score 151.5; DB 2; Length 228;
Best Local Similarity 24.6%; Pred. No. 6.9e-08;
Matches 62; Conservative 36; Mismatches 87; Indels 67; Gaps 11;

QY 132 HTETGNIWTHLLGFVL-----FLFLGILTMLRPNMYFMAPLOEKVV-FGMFFLGAIVLCLSF 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 HGERLNWATHLIGAVAACTGAVMLTVQASLNGSPW-----KIVGVGVYGVITLLLYSI 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 SWLPHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFYCSPQPRLIYLSIVCVLG 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 79 STAYHSVGRKAVVWR---KLDHLSIYLLIAGSYTP-----FC-----LVTLRG 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 ISAIIVAOQDRPATPKRQTRAGVFLGCLGSLGVVPTMHTIAGGFVKATTVGQMGWFFLM 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 -----PWG-----WTLFGIVMGLAVLGMLOEKIPRSEARVLSVVIYAVMGWIVLI 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 307 AVMYI-----TGAGLYAARIPERFPFGKFDIWFQSHQIFHVLVVAAPVHFY 353
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 165 AVKPLAALGAGFTWLAAGGVLYTVGVFYAIDHRFRHW---HGIWHLFVIAGSLLHPV 221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 354 GVSNLQEFYRGL 365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 AI-----WRYVL 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-270-767-46435
; Sequence 46435, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7325-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 46435
; LENGTH: 143

```

```

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46435

Query Match
Best Local Similarity 6.4%; Score 129; DB 2; Length 143;
Matches 36; Conservative 21; Mismatches 47; Indels 28; Gaps 5;

QY 223 WLYSPFCSPQRLIYLSIVCVLIGSIAIIVAQ--WDR---FATPKHQTRAGVFLGLGLS 277
DB 1 WLIIVSYC-----VLSLNGLYKALTASSPQWRLLCFALPFAMRS---ILTLRLR 47

QY 278 GVVPTMHFTIAGFVKATTVGQMGWFLMAVMYITGAGLYAARIPERFFPKFDIWFQSH 337
DB 48 GMVGGSHMALSHVYLQVEDG-----VSILGGAIGAMRIPEKWFPGVVDYLNH 97

QY 338 QIFHVLVVAAP 349
DB 98 NIMHVLVVAVY 109

```

```

RESULT 6
US-09-107-532A-4817
; Sequence 4817, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Walcham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 4817:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...234
; SEQUENCE DESCRIPTION: SEQ ID NO: 4817:
US-09-107-532A-4817

```

Query Match 6.1%; Score 122; DB 2; Length 234;

```

Best Local Similarity 24.1%; Pred. No. 0.00011;
Matches 59; Conservative 47; Mismatches 83; Indels 56; Gaps 15;

QY 125 FKSIFRIHTETGNIWTHLGLFVLFLFGLITMLRPNMFMAPLQEKVKVGMFPLGAVLCL 184
DB 23 FNRTEILLNEVFNATHGIGTGLSI-AGLVLLVKGALHSLH---IVSYAIYSGMML 78

QY 185 SP--SWLFHT-VYCHSEKVRFTSKLDYSGIALLMGSPV-----WLYSPFCSPQ 233
DB 79 LFLTSTLHSLIFTAKKVQVF---DHSSIFLLIAGSYTPFCLLSIRGLMGWTLF---- 131

QY 234 PRLIYLSIVCVLGI--SAIIVAQWDRFATPKHQTRAGVFLG-LGLSGVVPTMHFTIABG 290
DB 132 ---VLIIWLFALIGIYKALTLLHRRKRSKV---STIIIFMGWLCVVAAPLYH----- 179

QY 291 FVKATTVGQMGWFFLMA--VMYITGAGLYAARIPERFFPKFDIWFQSHOIFHVLV-VAA 347
DB 180 ----SLGWTGVILMVAGGLSYTIGA-----FFVSLNSIRYM-HVVWHLFVMLGA 223

QY 348 AFVHF 352
DB 224 GFWYF 228

```

```

RESULT 7
US-09-134-000C-3636
; Sequence 3636, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3636
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3636

```

```

Query Match 5.9%; Score 118.5; DB 2; Length 236;
Best Local Similarity 23.4%; Pred. No. 0.00026;
Matches 56; Conservative 42; Mismatches 92; Indels 49; Gaps 11;

QY 125 FKSIFRIHTETGNIWTHLGLFVLFLFGLITMLRPNMFMAPLQEKVKVGMFPLGAVLCL 184
DB 24 FSKKYLIVNEVLNAVTHGIGAGLSI-AGLVLLVKGALGSPH---VVSYAIYSGMML 79

QY 185 SP--SWLFHT-VYCHSEKVRFTSKLDYSGIALLMGSPV-----WLYSPFCSPQ 233
DB 80 LFLSTLHSLIFTAKKVQVF---DHSSIFLLIAGSYTPFCLLSIRGLMGWTLF---- 132

QY 234 PRLIYLSIVCVLGI--SAIIVAQWDRFATPKHQTRAGVFLGSLGSLGVVPTMHFTIABG 293
DB 133 ---SLVWLIATVIGIVYKSLTLHKQETVKIISTIIYIVLWLCIIAARPLYESLGT- 185

QY 294 ATTVGQMGWFFLMA--VMYITGAGLYAARIPERFFPKFDIWFQSHOIFHVLVVAAPV 350
DB 186 ----GTALLVAGGVSVTLGAAPFYSLK-----NVRFM-HVVWHLFVMLAAIL 226

```

```

RESULT 8
US-09-134-001C-4836
; Sequence 4836, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

```



```

QY 129 FRIHTETGNIWTHLLGFLVFLFGLILTMRLPNMYFMAPLOEKVVFQGMFFLGAVALCLSFWS 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 YSLAEVANSISHGIGLV-FGIVGLVLLVQAADTNASATAIASYSLYGGSMIMFLAST 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 LFTVTVCHSEKVSRTSKLDYSIGIALLIMSGFVWLYYSCFPQPRLLIVLSIVCVLGIS 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 LYHAI--PHORAKQWLKFDHCAIYLLIAGTYTFFL-----LVGLNSPLAKGLM 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 AIIVAOWDRPATPKHRQTRAGVFLGLGSLGVPWPTMHFTIAEGF--VKATTVGQMGWFFLM 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 IVI---W-----SLALLGIL--FKLTIAHRFKILSLVTLTWGMLSLI 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 307 -----AVMYITGAGLYAA-RIPERFFPKGFDIMFQSHQIFHVLVV 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 VYQLAVKLVAGVGTLLAVGGVYSLGVIFVCKRIP-----YNHAIWHRGFVL 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 346 AAAPVHPYGV 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 GGSVCHFLAI 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 12

US-09-902-540-14983
 ; Sequence 14983, Application US/09902540
 ; Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(15849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 14983
 LENGTH: 571
 TYPE: PRF
 ORGANISM: Myxococcus xanthus
 US-09-902-540-14983

Query Match 5.3%; Score 106; DB 2; Length 571;

Best Local Similarity 24.4%; Pred. No. 0.022;
 Matches 48; Conservative 32; Mismatches 69; Indels 48; Gaps 11;

```

QY 125 FKSIFRI-HTETGNIWTHLLGFLVFLFGLILT-----MLRPNMYFMAPLOEK---VVFQMF 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 FNSVHSFTQSDIGTPTFLVFLGLVLCVGLLAVRGLLPVPEGQLASPLSREASILVNNLV 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 FLGAVLCLSFSLFHTVY-----CHSEKVS---RTFSKLDY-SGIALIM--GSPVPW 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 F-----VAITFTVLLTGLTYPLISEAVHGVRSVSGSPYFNKMAVPGGIAVFLMVGVPVLPW 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 LYSYFSCFPQPRLLIVLSIVCVLGISALIIVAOWDRFATPKHRQTRAGVFLGLGSLGVVPTM 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 -----GKPDPAUURRQFIPSVVGLVTTA-----ACPAVGLRGVYPLM 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 284 HFTIAEGFVKATTVGOM 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 TFGLA-GFVTVTVREL 366
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13

US-09-583-110-3435
 ; Sequence 3435, Application US/09583110
 ; Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

```

; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3435
; LENGTH: 215
; TYPE: PRF
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-3435

Query Match 5.2%; Score 105; DB 2; Length 215;
Best Local Similarity 20.1%; Pred. No. 0.0066;
Matches 52; Conservative 38; Mismatches 69; Indels 100; Gaps 13;

QY 134 ETGNIWTHLLGFLVFLF-----GILTLRPNMYFMAPLOEKVVFQGMFFLGA 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 16 ETANSVTHAVGAVIMLILLPISSIYSYEAHGLSSIGVSIF-----V 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 LCLSFSLFHTVYCHSEKVSRTFSK-----LDYSGIALLIMSGFVP-----WLYYSFY 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 ISLFLMFLSSTIY-HSMAYGSTHKYVLRIRIHDHSMIYVAIAGSYTPVVLTMNNWFGY--- 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 CSPQPRLLIVLSIVCVLGISALIIVAOWDR-----FATPKHRQTRAGVFLGLG--LSG 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 -----LIIIVHGWTFITGLTKIFAINVNDKESLALYLMGWLVA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 VVPTMHFTIAEGFVKATTVGQMGWFFLM--AVMYITGAGLYAARIPERFFPKGFDIWFQS 336
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 155 IIPAI-----INQTT--PVFWSLMVTVGGLCYTVGAGFYAKKDP--YF----- 192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 337 HQIFHVLVVAAAPVHPYGV 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 HMIWHLFILAAASVLQYIAI 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14

US-09-107-433-2676
 ; Sequence 2676, Application US/09107433
 ; Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
 THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSER: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

```

;
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-011
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 2676:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 233 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     HYPOTHETICAL: YES
;     ORIGINAL SOURCE:
;       ORGANISM: Streptococcus pneumoniae
;     FEATURE:
;       NAME/KEY: misc_feature
;       LOCATION: (B) LOCATION 1...233
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2676:
US-09-107-433-2676

```

```

Query Match      5.2%; Score 105; DB 2; Length 233;
Best Local Similarity 20.1%; Pred. No. 0.0074;
Matches 52; Conservative 38; Mismatches 69; Indels 100; Gaps 13;

QY 134 ETGNIWTHLGGVLEFLP-----GILTMLRPNMYFMAPLQEKVVFGMFFLGAV 181
DB 34 EIANSTHAGVIMLILPISIIYSYEAHGLSSIGVSIF-----V 75

QY 182 LCLSFSLFHTVYCHSEKVSRTFSK----LDYSGIALLIMSGFVP-----WLYYSFY 229
DB 76 ISLFLMPLSSTIY-HSMAYGSTHKYVLRILIDHSMIYVAIAGSYTPVVLTLNNWFGY--- 131

QY 230 CSPQRLIYLSIVCVLGISAIIVAQWDR-----FATPKHQRTAGVFLGLG--LSG 278
DB 132 -----LIIIVHMGTTIFGTLYKIFAINVNDKFSLLALYLIMGLVLA 172

QY 279 VVPTMHTTIAEGFVKATTVGQMGWFFLM--AVMYITGAGLYAARIPEPFPGKFDIWFOS 336
DB 173 IIPAI-----INQTT--PVFWSLMVYGGLCYTVGAGFYAKKP--YF----- 210

QY 337 HQIFHVLVVAAFVHFYGV 355
DB 211 HMIWHLFILAASVLQVIAI 229

```

```

RESULT 15
US-09-489-039A-8942
; Sequence 8942, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8942
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8942

```

```

Query Match      5.2%; Score 104; DB 2; Length 722;
Best Local Similarity 23.5%; Pred. No. 0.052;
Matches 77; Conservative 43; Mismatches 123; Indels 84; Gaps 16;

QY 63 EVRVLTLPLOAHMKMEEFVYKVGWRWRVIPYDVLPDW-----LKN--DYLLHGR 115
DB 228 EVSVIGIVL-----LVASIWFG--GVIAHD--PYWGPALTFKDTTITFTLIGY- 271

```

Search completed: April 19, 2006, 14:04:35
Job time : 38.2774 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rapn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rnpm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

This Page Blank (uspto)

GenCore version 5.1.7
Copyright, (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2006, 14:20:09 ; Search time 20.5861 Seconds
(without alignments)
801.567 Million cell updates/sec

Title: US-10-799-943-2
Perfect score: 2009
Sequence: 1 MSHKGSVVAQNGAPASNR.....SNLQEPFRYGLGCTDDTL 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 4402918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
5: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	29.6	318	7	US-11-188-298-16712
2	530.5	26.4	324	7	US-11-188-298-7728
3	515	25.6	315	7	US-11-188-298-6654
4	479.5	23.9	376	7	US-11-096-568A-11895
5	479.5	23.9	406	7	US-11-096-568A-11894
6	479	23.8	329	7	US-11-188-298-17246
7	477	23.7	324	7	US-11-096-568A-17089
8	477	23.7	345	7	US-11-096-568A-17088
9	477	23.7	371	7	US-11-096-568A-17087
10	474	23.6	317	7	US-11-188-298-21152
11	474	23.6	327	7	US-11-188-298-7868
12	468	23.3	328	7	US-11-188-298-13492
13	453.5	22.6	380	7	US-11-096-568A-22007
14	453.5	22.6	426	7	US-11-096-568A-22006
15	451.5	22.5	332	7	US-11-188-298-326
16	445	22.2	263	7	US-11-188-298-15865
17	437	21.8	387	7	US-11-096-568A-27407
18	437	21.8	405	7	US-11-096-568A-27406
19	431	21.5	374	7	US-11-096-568A-27408
20	425	21.2	317	7	US-11-188-298-15303
21	416.5	20.7	351	7	US-11-096-568A-26845
22	407	20.3	316	7	US-11-188-298-12382
23	399	19.9	316	7	US-11-188-298-9290
24	377	18.8	497	7	US-11-188-298-2733
25	373.5	18.6	215	7	US-11-096-568A-26847

26	373.5	18.6	252	7	US-11-096-568A-26846	Sequence 26846, A
27	372	18.5	442	7	US-11-188-298-13605	Sequence 13605, A
28	357	17.8	221	7	US-11-096-568A-22008	Sequence 22008, A
29	356	17.7	498	7	US-11-188-298-1166	Sequence 1166, Ap
30	336.5	16.7	490	7	US-11-188-298-2544	Sequence 2544, Ap
31	318.5	15.9	822	7	US-11-188-298-6572	Sequence 6572, Ap
32	269	13.4	467	7	US-11-096-568A-19600	Sequence 19600, A
33	269	13.4	476	7	US-11-096-568A-19599	Sequence 19599, A
34	261	13.0	401	7	US-11-096-568A-19601	Sequence 19601, A
35	252	12.5	419	7	US-11-188-298-1381	Sequence 1381, Ap
36	251	12.5	543	7	US-11-188-298-21359	Sequence 21359, A
37	204.5	10.2	346	5	US-09-978-360A-537	Sequence 537, App
38	176	8.8	137	6	US-10-644-807-409	Sequence 409, App
39	164	8.2	199	7	US-11-072-512-2886	Sequence 2886, Ap
40	137.5	6.8	210	7	US-11-045-004-1082	Sequence 1082, Ap
41	114.5	5.7	227	6	US-10-793-626-2642	Sequence 2642, Ap
42	111.5	5.6	354	7	US-11-188-298-13845	Sequence 13845, A
43	107.5	5.4	448	7	US-11-087-099-10069	Sequence 10069, A
44	100.5	5.0	464	7	US-11-087-099-8095	Sequence 8095, Ap
45	100	5.0	258	7	US-11-096-568A-30003	Sequence 30003, A

ALIGNMENTS

RESULT 1

US-11-188-298-16712
; Sequence 16712, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Aaad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16712
; LENGTH: 318
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-16712

Query Match 29.6%; Score 595; DB 7; Length 318;
Best Local Similarity 43.0%; Pred. No. 1e-45;
Matches 122; Conservative 46; Mismatches 102; Indels 14; Gaps 4;

Qy	94	VIPIYVLPDWLKDNDVLLHGRPPMPSPFRACFKSIPIRIHTETGNIWTHLLGFLFLGI	153
Db	39	LVHWDELPHWQRDNQIHITGYRPASYSFRGSFQSLTYIHNETVNIYTHLLPSVLAIPAAI	98
Qy	154	LTMRLPNMY-FWAPLOEKV-----VFGMFFLGAVLCLSFSLFHTVYCHSEKVSRTFSK	206
Db	99	-----OLYRALAPRYETATDGIAPGCFVGAACLGMSAFYHTISHNSPTVAIGNT	152
Qy	207	LDYSGIALIMSGSEFVFWLYSYFYCSPQRLIYLISIVCVLGISAIIVQMDRFPATPKHQRT	266
Db	153	FDYIGIVGLVGSFVSVYVYGFYCVPELQRLYWSMCTIGLGCIVVSIIPKFTPRWRPF	212
Qy	267	RAGVFVGLGLSGVVPVTHFTIAGFVKATVVGQMGHFFLMVNVYITGAGLYAARIPIRPF	326
Db	213	RAAMFVGMGLSAPFVVPVHGLYGRDQMRQIQLGHLQLLQGGFLYILGAGIYAARVPERLR	272
Qy	327	PGKEDVWFQSHQIFHVLVVAAPVHFYGVSNLQEFY-GLEGGC	369
Db	273	PGGFDLWGSQSHQIFHVLVWCAVAHVTGLLRAPDFRHNRTAGSC	316

RESULT 2

US-11-188-298-7728
; Sequence 7728, Application US/11188298
; Publication No. US20060075522A1

NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 11894
LENGTH: 406
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(406)
OTHER INFORMATION: Ceres Seq. ID no. 13658849
US-11-096-568A-11894

Query Match 23.9%; Score 479.5; DB 7; Length 406;
Best Local Similarity 34.7%; Pred. No. 3.1e-35;
Matches 115; Conservative 48; Mismatches 99; Indels 69; Gaps 7;

QY 91 RW-----RVTPYDVLDPWLKNDYLLHGHPPMPSFRACPKSIFRIHTETGNIWTHLLGF 145
DB 81 RWAGGLPRLKRFBELPDYLDNDEFIRGGYKCEW-SVRDALRSVFAWHNETLNWTHLLGGF 139
QY 146 VLFLFL-----GILTM-----LRPNMYFMAPLOEKVVF----- 174
DB 140 FLFLGLAVAGQETWRPAGAAAAGFTWMTWSANASSLATNNSSTAIQSALASGIGGAG 199
QY 175 -----MFFLGAVLCISFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWY 225
DB 200 HAVARWPRTVFLGAMTCLSVSAAHLLASHRRNRLFWOLDYAGIAMVIVASFFPPVY 259
QY 226 YSFYCSPOPRLIYLSVCLGISAIIIVAQWDRFATPKHROTGRAGVFLGLSGVPTMHF 285
DB 260 YTEFGSPVAQLAYLSAITLLGLVVAALLVPARSSPRLRLHLAGLVSMGLSGVVPALHA 319
QY 286 TIAEGFVKATTVGOMG-----PFLMAVMYITGAGLYAARIPIRFFPKGKDIWF 334
DB 320 L-----WLNWGHCECYLAISLELAMLGLVATGATGVVARVPERWRFGMEDCVG 367
QY 335 QSHQIHFVLVVAAPVHFYGVSNLOEFYGL 365
DB 368 HSHQIHFVLVVGAVTHYAATAILIGWRDAL 398

RESULT 6
US-11-188-298-17246
Sequence 17246, Application US/11188298
Publication No. US20060075522A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 17246
LENGTH: 329
TYPE: PRT
ORGANISM: Eremothecium gossypii
US-11-188-298-17246

Query Match 23.8%; Score 479; DB 7; Length 329;
Best Local Similarity 38.0%; Pred. No. 2.7e-35;
Matches 97; Conservative 53; Mismatches 105; Indels 0; Gaps 0;

QY 97 YDVLDPWLKNDYLLHGHPPMPSFRACPKSIFRIHTETGNIWTHLLGLFVFLGLTLTM 156
DB 55 WDDLDPDQKDNHILSGYVRETSYRKTFRSLFYLHNESVNIYSHLIPGICFLFIALFNK 114
QY 157 LRPNMYFMAPLOEKVVFMEFLGAVLCISFSLFHTVYCHSEKVSRTFSKLDYSGIALLI 216
DB 115 YVADYETTTWKYIMDIDIFLLGAVVCLTILSGVTHCKWSLSEVSFGNKLDIGIVALLI 174
QY 217 MGSFVPMWLYSYFCSPOPRLIYLSIVCLGISAIIVAQWDRFATPKHROTGRAGVFLGL 276

DB 175 SCMSIQMYGYDYDSTAMPFSLSTVTLSLALACAVVLSLPHRSREWRKYRAAIFTAFGL 234
QY 277 SGCVPTMFTTAEAGFVKATTVGQMGFFLMAVYITGAGLYAARIPIRFFPKGKDIWFOS 336
DB 235 SGLLPVITSCFYGYPIEAYSRIQLKWLSEGLVYISGAVLYGVRPPEKLEPGSFDIWHGS 294
QY 337 HQIFHVLVVAAPVH 351
DB 295 HQIFHVLVVAALCH 309

RESULT 7

US-11-096-568A-17089
Sequence 17089, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 17089
LENGTH: 324
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(324)
OTHER INFORMATION: Ceres Seq. ID no. 12356019
US-11-096-568A-17089

Query Match 23.7%; Score 477; DB 7; Length 324;

Best Local Similarity 35.3%; Pred. No. 4e-35;

Matches 109; Conservative 53; Mismatches 115; Indels 32; Gaps 5;

QY 91 RWRVIPYDVLDPWLKNDYLLHGHPPMPSFRACPKSIFRIHTETGNIWTHLLGLFVFLF 150
DB 13 RPRLVGYBELPEVLKONEYIRGHYRAEW-VRDALLSAPAWHNETLNWTHLLGGFLFFLA 71

QY 151 LGILTMRLPNMYFMAP-LOEKV-----FG-----MFPLGA 180
DB 72 LAVAGGRKEADGAAPGIMRFVVRLDWSGSDHPQRHDDAGASLPSVPRWRTVFLVGA 131

QY 181 VLCLSFSLFHTVYCHSEKVSRTFSKLDYSGIALLIMSGFVPMWLYSYFCSPOPRLIYLS 240
DB 132 MSCLAISAAHLLACHSRASAVFWOLDYAGISVMIVASFVPPVYAFVFLCHPPARAAYLC 191

QY 241 IVCVLGISAIIVAQWDRFATPKHROTGRAGVFLGLSGVVPWTHFTIAGSFVKATTGQM 300
DB 192 AIAALGALVVAALLSPSCSSPRYRLRAALFLAMGLSGVVPVPAH-ALMLNWGHAACYLAL 250

QY 301 GMFFLMAVMYITGAGLYAARIPIRFFPKGKDIWFQSHQIFHVLVVAAPVHFYGVSNLOE 360
DB 251 GIEVVMGLTYATGAWFYVSRVPEKWRPGVDVVGSHQIFHVLVVGAVTHYVAVAVLIH 310

QY 361 FRYGLEGGC 369

DB 311 WREKVAVAC 319

RESULT 8

US-11-096-568A-17088
Sequence 17088, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01

```
/ NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17088
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(345)
; OTHER INFORMATION: Ceres Seq. ID no. 12356018
;
US-11-096-568A-17088

Query Match      23.7%; Score 477; DB 7; Length 345;
Best Local Similarity 35.3%; Pred. No. 4.7e-35;
Matches 109; Conservative 53; Mismatches 115; Indels 32; Gaps 5;

QY 91 RWRVIVDVLVDLWLVKNDYLLHGRPPMPSPFRACFKSIPIRIHTETGNIWTHLLGFLVFLF 150
Db 34 RPLVGYEELPEYLKONETIRGHYRAEWP-VRDALLSAFAWNETLNVWTHLGGFLFFLA 92
QY 151 LGILTMLRPNMYPMP-LOEKVV-----FG-----MFFLGA 180
Db 93 LAVAGRKEAADAAGIIMRFVVRDLSWGSDDHPCQPRHDDAGASLSPVRPRTVFLVGA 152
QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYSYFYCSPQPRLIYLS 240
Db 153 MSCLAISAAAHLLACHSRASAVFWQLDYAGISVMIVASFVPPVYAFCLCHPPARAAYLC 212
QY 241 IVCVLGISAIIVAOQWDRFATPKHQTRAGVFLGLGSLGVVPTMHTIAGFVKATTVGQM 300
Db 213 ATAAALGALVVAALLSPSCSPRYRRLRAALFLAMGLSGVVPALH-ALWLNMGHAAACYLAL 271
QY 301 GWFFLMAVMYITGAGLYAARIPERFPFGKFDIWFQSHOIFHVLVVAAPVHFYGVSNLQ 360
Db 272 GIEVVMGLTYATGAWFYVSRVPEKWRPGVDVGVGSHQIFHVLVLVGAVTHVAVAVLIH 331
QY 361 FRYGLEGGC 369
Db 332 WREKVAVAC 340

RESULT 9
US-11-096-568A-17087
; Sequence 17087, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17087
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(371)
; OTHER INFORMATION: Ceres Seq. ID no. 12356017
;
US-11-096-568A-17087

Query Match      23.7%; Score 477; DB 7; Length 371;
Best Local Similarity 35.3%; Pred. No. 4.7e-35;
Matches 109; Conservative 53; Mismatches 115; Indels 32; Gaps 5;

QY 91 RWRVIVDVLVDLWLVKNDYLLHGRPPMPSPFRACFKSIPIRIHTETGNIWTHLLGFLVFLF 150
Db 60 RPLVGYEELPEYLKONETIRGHYRAEWP-VRDALLSAFAWNETLNVWTHLGGFLFFLA 118
QY 151 LGILTMLRPNMYPMP-LOEKVV-----FG-----MFFLGA 180
Db 119 LAVAGRKEAADAAGIIMRFVVRDLSWGSDDHPCQPRHDDAGASLSPVRPRTVFLVGA 178
```

```
QY 181 VLCLSFSLFHTVYCHSEKSVRTFSKLDYSGIALLIMSGFVPMWLYSYFYCSPQPRLIYLS 240
Db 179 MSCLAISAAAHLLACHSRASAVFWQLDYAGISVMIVASFVPPVYAFCLCHPPARAAYLC 238
QY 241 IVCVLGISAIIVAOQWDRFATPKHQTRAGVFLGLGSLGVVPTMHTIAGFVKATTVGQM 300
Db 239 ATAAALGALVVAALLSPSCSPRYRRLRAALFLAMGLSGVVPALH-ALWLNMGHAAACYLAL 297
QY 301 GWFFLMAVMYITGAGLYAARIPERFPFGKFDIWFQSHOIFHVLVVAAPVHFYGVSNLQ 360
Db 298 GIEVVMGLTYATGAWFYVSRVPEKWRPGVDVGVGSHQIFHVLVLVGAVTHVAVAVLIH 357
QY 361 FRYGLEGGC 369
Db 358 WREKVAVAC 366

RESULT 10
US-11-188-298-21152
; Sequence 21152, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 21152
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
;
US-11-188-298-21152

Query Match      23.6%; Score 474; DB 7; Length 317;
Best Local Similarity 38.4%; Pred. No. 7.2e-35;
Matches 104; Conservative 45; Mismatches 116; Indels 6; Gaps 2;

QY 93 RVIPYDVLVDLWLVKNDYLLHGRPPMPSPFRACFKSIPIRIHTETGNIWTHLLGFLVFL 149
Db 38 RLYSWDEIPEQWRNDLHGVVKTETSFIEFKSLFYLHNESVNIYSHLIPALGFTVL 97
QY 150 FLGILTMLRPNMYPMP-LOEKVVFWGMFPLGAVLCLSPSLFHTVYCHSEKSVRTFSKLDY 209
Db 98 LLDKSTI---KVFATTTWLDHMDIDLFYSGAFACILSSSFCLKSHSLRIATLGNKLDY 154
QY 210 SGIIALLIMSGFVPMWLYSYFYCSPQPRLIYLSIVCVLGISAIIVAOQWDRFATPKHQTRAG 269
Db 155 LGICILIVTSVMVSIYGYPEKPSLFCLPALITVSFGIACSVSLKDKFKREMPYRAG 214
QY 270 VFLGLGSLGVVPTMHTIAGFVKATTVGQMGWFLMAVMYITGAGLYAARIPERFPFGK 329
Db 215 LFVCFGLSSIPIFSGLYCSFSFIWTQIQLFWLLGGVLYIGAVLGYIMRPFPEKICPGK 274
QY 330 FDIWFQSHOIFHVLVVAAPVHFYGVSNLQ 360
Db 275 FDIWGHSHQLFHLVAVIAALCHLRGLLSYE 305

RESULT 11
US-11-188-298-7868
; Sequence 7868, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
```


QY 318 AARIPERFFPGKFDIWFQSHQIFHVLVAAAFVHFYGVSNLQEFFRYGLEGGCTDDL 374

